· OM nucleic - nucleic search, using sw model

Run on:

November 7, 2007, 02:11:02; Search time 3283 Seconds

(without alignments)

10209.126 Million cell updates/sec

Title:

US-10-529-319-1

Perfect score: 4494.2

Sequence:

1 tcatacttttagagtcagat.....tcaccgctcattccagacac 4523

Scoring table: IDENTITY NUCDX

Gapop 10.0 , Gapext 1.0

Searched:

5620219 seqs, 3705283702 residues

Total number of hits satisfying chosen parameters:

11240438

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N\_Geneseq\_200701:\*

1: geneseqn1980s:\*

2: geneseqn1990s:\*

3: geneseqn2000s:\*

4: geneseqn2001as:\*

5: geneseqn2001bs:\*

6: geneseqn2002as:\*

7: geneseqn2002bs:\*

8: geneseqn2003as:\*

9: geneseqn2003bs:\*

10: geneseqn2003cs:\*

11: geneseqn2003ds:\*

12: geneseqn2004as:\*

13: geneseqn2004bs:\*

14: geneseqn2005s:\*

15: geneseqn2006s:\*

16: geneseqn2007s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	% Query Match	Length	DB	1D	Description
1	4494 2	100 0	4523	12	ΔD032292	Ado32292 Bacterial

OM nucleic - nucleic search, using sw model

November 7, 2007, 02:11:02; Search time 15 Seconds Run on:

(without alignments)

10209.126 Million cell updates/sec

US-10-529-319-6 Title:

Perfect score: 18.8

1 aarytnggmcctgaagaaat 20 Sequence:

Scoring table: IDENTITY NUCDX

Gapop 10.0 , Gapext 1.0

5620219 seqs, 3705283702 residues Searched:

Total number of hits satisfying chosen parameters: 11240438

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

N Geneseq 200701:\* Database :

1: geneseqn1980s:\*

2: geneseqn1990s:\*

3: genesegn2000s:\*

4: geneseqn2001as:\*

5: genesegn2001bs:\*

6: genesegn2002as:\*

7: geneseqn2002bs:\*

8: geneseqn2003as:\*

9: geneseqn2003bs:\*

10: geneseqn2003cs:\*

11: genesegn2003ds:\* 12: geneseqn2004as:\*

13: geneseqn2004bs:\*

14: geneseqn2005s:\*

15: geneseqn2006s:\*

16: geneseqn2007s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	DB	ID	Description
1	18.8	100.0	20	12	AD032297	Ado32297 Bacterial

OM nucleic - nucleic search, using sw model

Run on: November 7, 2007, 02:11:02; Search time 17 Seconds

(without alignments)

10209.126 Million cell updates/sec

Title: US-10-529-319-7

Perfect score: 22.2

Sequence: 1 tgnartttrtcatcaaccatgtg 23

Scoring table: IDENTITY NUCDX

Gapop 10.0 , Gapext 1.0

Searched: 5620219 seqs, 3705283702 residues

Total number of hits satisfying chosen parameters: 11240438

Minimum DB seg length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100%

Listing first 45 summaries

Database: N Geneseq 200701:\*

1: geneseqn1980s:\*

2: geneseqn1990s:\*

3: geneseqn2000s:\*

4: geneseqn2001as:\*

5: geneseqn2001bs:\*

6: geneseqn2002as:\*

7: geneseqn2002bs:\*

8: geneseqn2003as:\*

9: geneseqn2003bs:\*

10: geneseqn2003cs:\*

11: geneseqn2003ds:\*

12: geneseqn2004as:\*

13: geneseqn2004bs:\*

14: geneseqn2005s:\*

15: geneseqn2006s:\*

16: geneseqn2007s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	DB	ID	Description
1	22.2	100.0	23	12	AD032340	Ado32340 Bacterial

My 8

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OM nucleic - nucleic search, using sw model

Run on: November 7, 2007, 02:11:02; Search time 515 Seconds

(without alignments)

10209.126 Million cell updates/sec

Title: US-10-529-319-8

Perfect score: 709

Sequence: 1 cgcgaaattccaaacgttgg.....tcaccacatggttgatgaca 709

Scoring table: IDENTITY NUCDX

Gapop 10.0 , Gapext 1.0

Searched: 5620219 seqs, 3705283702 residues

Total number of hits satisfying chosen parameters: 11240438

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: N Geneseq 200701:\*

1: · geneseqn1980s:\*

2: geneseqn1990s:\*

3: geneseqn2000s:\*

4: geneseqn2001as:\*

5: geneseqn2001bs:\*

6: geneseqn2002as:\*

7: geneseqn2002bs:\*

8: geneseqn2003as:\*

9: geneseqn2003bs:\*

10: geneseqn2003cs:\*

11: geneseqn2003ds:\*

12: geneseqn2004as:\*

13: geneseqn2004bs:\*

14: geneseqn2005s:\* 15: geneseqn2006s:\*

16: geneseqn2007s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	% Query Match	Length	DB	ID	Description
1	<b>-</b> 709	100.0	709	12	ADO32299	Ado32299 Bacterial

OM nucleic - nucleic search, using sw model

Run on: November 7, 2007, 02:12:55; Search time 29158 Seconds

(without alignments)

10721.919 Million cell updates/sec

Title: US-10-529-319-1

Perfect score: 4494.2

Sequence: 1 tcatacttttagagtcagat.....tcaccgctcattccagacac 4523

Scoring table: IDENTITY NUCDX

Gapop 10.0 , Gapext 1.0

Searched: 7568541 seqs, 34560148153 residues

Total number of hits satisfying chosen parameters: 15137082

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl:\*

1: gb\_env:\*

2: gb\_pat:\*

3: gb ph:\*

4: gb pl:\*

5: gb\_pr:\*

6: gb\_ro:\*

7: gb sts:\*

8: gb\_sy:\*

9: gb un:\*

10: gb\_vi:\*

11: qb ov:\*

12: gb htg:\*

13: gb\_in:\*

14: gb\_om:\*

15: gb\_ba:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	% Query Match	Length	DB	ID	Description
1 2		100.0			CQ816375 AF535183	CQ816375 Sequence AF535183 Streptoco

rge-6

GenCore version 6.2.1
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OM nucleic - nucleic search, using sw model

Run on: November 7, 2007, 02:12:55; Search time 129 Seconds

(without alignments)

10721.919 Million cell updates/sec

Title: US-10-529-319-6

Perfect score: 18.8

Sequence: 1 aarytnggmcctgaagaaat 20

Scoring table: IDENTITY NUCDX

Gapop 10.0 , Gapext 1.0

Searched: 7568541 seqs, 34560148153 residues

Total number of hits satisfying chosen parameters: 15137082

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl:\*

1: gb\_env:\*
2: gb\_pat:\*
3: gb\_ph:\*
4: gb\_pl:\*

5: gb\_pr:\*
6: gb\_ro:\*
7: gb sts:\*

8: gb\_sy:\*

9: gb\_un:\*

10: gb\_vi:\*
11: gb ov:\*

12: gb\_0v.

13: gb\_in:\*

14: gb\_om:\*

15: gb\_ba:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	% Query Match	Length	DB	ID	Description	
1	18.8	100.0	20	2	CQ816380	CQ816380 Sequence	
2	18.8	100.0	763	2	AX414438	AX414438 Sequence	

OM nucleic - nucleic search, using sw model

Run on: November 7, 2007, 02:12:55; Search time 148 Seconds

(without alignments)

10721.919 Million cell updates/sec

Title: US-10-529-319-7

Perfect score: 22.2

Sequence: 1 tgnartttrtcatcaaccatgtg 23

Scoring table: IDENTITY NUCDX

Gapop 10.0 , Gapext 1.0

Searched: 7568541 seqs, 34560148153 residues

Total number of hits satisfying chosen parameters: 15137082

Minimum DB seg length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl:\*

1: gb\_env:\*

2: gb\_pat:\*

3: gb\_ph:\*

4: gb pl:\*

5: gb pr:\*

6: gb\_ro:\*

7: gb sts:\*

8: gb\_sy:\*

9: gb\_un:\*

10: gb\_vi:\*

11: gb\_ov:\*

12: gb\_htg:\*

13: gb in:\*

14: gb\_om:\*

15: gb\_ba:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

 ult No.	Score	% Query Match	Length	DB	ID	 Description
 1 2		100.0			CQ816381 CO816423	CQ816381 Sequence CQ816423 Sequence

OM nucleic - nucleic search, using sw model

November 7, 2007, 02:12:55; Search time 4571 Seconds Run on:

(without alignments)

10721.919 Million cell updates/sec

US-10-529-319-8 Title:

Perfect score: 709

1 cgcgaaattccaaacgttgg.....tcaccacatggttgatgaca 709 Sequence:

IDENTITY NUCDX Scoring table:

Gapop 10.0 , Gapext 1.0

7568541 seqs, 34560148153 residues Searched:

Total number of hits satisfying chosen parameters: 15137082

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl: \*

1: gb env:\*

2: gb\_pat:\*

3: gb ph:\*

4: gb pl:\*

gb pr:\* 5:

qb ro:\* 6:

7: gb sts:\*

8: gb sy:\* 9: gb un:\*

10: gb vi:\*

11: gb\_ov:\*

12: gb htg:\*

13: gb\_in:\*

14: gb\_om:\*

15: gb\_ba:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	DB	ID	Description
1	709 693	100.0 97.7		_	CQ816382 AF535171	CQ816382 Sequence AF535171 Streptoco

OM nucleic - nucleic search, using sw model

Run on: November 7, 2007, 02:15:04; Search time 17684 Seconds

(without alignments)

15868.232 Million cell updates/sec

Title: US-10-529-319-1

Perfect score: 4494.2

Sequence: 1 tcatacttttagagtcagat.....tcaccgctcattccagacac 4523

Scoring table: IDENTITY NUCDX

Gapop 10.0 , Gapext 1.0

Searched: 53585215 seqs, 31020513797 residues

Total number of hits satisfying chosen parameters: 107170430

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : EST:\*

1: gb\_est1:\* 2: gb est3:\* 3: gb est4:\* 4: gb est5:\* 5: gb est6:\* gb htc:\* 6: 7: gb est2:\* 8: gb est7:\* 9: gb\_est8:\* 10: qb est9:\* 11: gb est13:\* 12: gb est12:\* 13: gb\_estl1:\* 14: gb\_estl0:\* 15: gb\_gssl:\* 16: gb gss2:\* 17: gb\_gss3:\*

18: gb\_gss4:\* 19: gb\_gss5:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,

SUMMARIES

and is derived by analysis of the total score distribution.

Result Query



1 1327 29.5 2768 16 BH770908 BH770908 LLMGtag64 2 295.2 6.6 3228 17 CL955048 CL955048 OJRMAN000 C 3 280 6.2 1037 18 DU758598 DU758598 ASNC2002. 4 262 5.8 1026 18 DU780806 DU780806 ASNB3401. C 5 254.2 5.7 979 18 DU742577 DU742577 SNC1288. C 6 239.4 5.3 1021 18 DU739640 DU739640 APKI5317. C 7 235.2 5.2 721 16 BZ560602 BZ560602 PZ622-164 DU762284 DU762284 ASNC4109. 9 228.8 5.1 1009 18 DU761500 DU761500 ASNC3728. C 12 216.2 4.8 1044 18 DU776284 ASNC4108. 11 217 4.8 988 18 DU766745 DU7767524 ASNC4128. C 12 216.2 4.8 1044 18 DU776982 DU7767828 ASNE4122. C 12 216.2 4.8 1044 18 DU776982 DU7767892 ASNB4122. C 12 12.2 4.7 527 19 AG947500 AG947500 DU766745 ANIW13628 ASNB4129. 15 212.8 4.7 596 19 AG947500 AG947500 DU766745 DU766745 DU766745 DU766745 DU766745 DU766745 ANIW13628 ASNB4129. C 12 18 197 4.4 1143 16 BZ579071 BZ5		No.	Score	Match	Length	DB	ID	Description
C 3 280 6.2 1037 18 DU758598 DU758598 ASNG2002. 4 262 5.8 1026 18 DU780806 DU780806 ASXB3401. C 5 254.2 5.7 979 18 DU742577 DU742577 ASNC1288. C 6 239.4 5.3 1021 18 DU739640 DU739640 APK15317. C 7 235.2 5.2 721 16 BZ560602 BZ560602 pacs2-164 8 233.2 5.2 1014 18 DU762284 DU762284 ASNG4109. 9 228.8 5.1 1009 18 DU761500 DU761500 ASNG3728. 10 222.8 5.0 682 19 AG275418 AG275418 Cyanidios 11 217 4.8 988 18 DU766745 DU7676745 ANIW13628 C 12 216.2 4.8 1044 18 DU776982 DU776982 ASXB1422. 13 214 4.8 590 19 AG947552 AG947950 Drosophil 14 213.2 4.7 527 19 AG947500 AG947500 Drosophil 15 212.8 4.7 696 19 AG947500 AG937500 Drosophil 16 210.2 4.7 1204 18 ED033682 ED033682 LD01_RA 17 200.8 4.5 614 19 AG935813 AG935813 Drosophil 16 210.2 4.7 14 652 15 AQ990247 AQ990247 Rfc00981 19 197 4.4 652 15 AQ990247 AQ990247 Rfc00983 19 197 4.4 1143 16 BZ579071 BZ579071 MSh2 6169 20 196.4 4.4 737 19 AG270164 AG270164 Cyanidios 21 195.2 4.3 589 18 DU769412 DU769412 APKG1440. 22 194.4 4.3 936 18 DU776912 DU769412 APKG1440. 24 188 4.2 783 17 CL686610 CL686610 RD104403 ASNG3751. 25 21 180.2 4.0 633 17 CL686610 CL686610 RD104438.b 26 180.2 4.0 633 17 CG896388 CG89638 PASB1402. 27 180.2 4.0 633 17 CG896380 CG89638 PASB1402. 28 180.2 4.0 633 17 CG896610 CL686610 RD104438.b 29 180.4 4.0 777 13 DN257460 DN257460 MS029717 31 179.2 4.0 633 17 CG896610 CL686610 RD104438.b 31 179.2 4.0 633 17 CG896610 CL686610 RD104438.b 31 179.2 4.0 837 2 BG302377 BG302377 IR-500-2 33 177.4 3.9 963 18 DU75813 DU75813 ASNF1671. 31 179.2 4.0 837 2 BG302377 BG302377 BG302377 IR-500-2 33 174.4 3.9 963 18 DU782018 DU758748 DU758748 ASNB2090. 34 174.4 3.9 979 18 CZ533942 CZ533942 SRAA-aac8 34 174.4 3.8 868 18 DU782058 DU732151 APK11587.		1	1327	29.5	2768	1.6	вн770908	BH770908 LLMGtag64
4         262         5.8         1026         18         D0780806         D0780806         ASXB3401.           C         5         254.2         5.7         979         18         D0739640         DU739640         APK15317.           C         7         235.2         5.2         721         16         BZ560602         BZ560602         BZ560602         D2762284         ASK84119.           9         228.8         5.1         1009         18         D0761500         DU761500         ASK9610.9         D2766745         D0766745         D0766745         ANGA75418         AGC75418         AGC75418         CAC75418         CAC7747         CAC76475         D0766745         D0766745         D0766745         D0766745         D0766745         D0766745         D0766745         ANGA77952         D0767982         AGS47952         D0767982         D0776982         D0776982         D0776982         D0776982         D0767992         D0769011         16         213.2         4.7         7696         19         AG939210         AG947950         D0769011         D076911 <t< td=""><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td>-</td></t<>								-
4         262         5.8         1026         18         D0780806         D0780806         ASXB3401.           C         5         254.2         5.7         979         18         D0739640         DU739640 APKI5317.           C         7         235.2         5.2         721         16         BZ560602         BZ560602 pacs2-164           8         233.2         5.2         1014         18         D0761500         D0762284         ASM64109.           9         228.8         5.1         1009         18         D0761500         D0761500 ASNG3728.           10         222.8         5.0         662         19         AG275418         AG275418 Cyanidios           11         212.4         4.8         1044         18         D0766745         D0766745 ANIWIJA628           13         214         4.8         590         19         AG947550         AG947952 Drosophil           14         213.2         4.7         527         19         AG947550         AG947952 Drosophil           15         212.8         4.7         696         19         AG93210         AG93210 Drosophil           16         210.2         4.7         1204         18	С		280	6.2		1.8		DU758598 ASNG2002.
C         5         254.2         5.7         979         18         DU742577         DU742577         ASNC1288.           C         6         239.4         5.3         1021         18         DU739640         DU739640         DU76284         DU762284           8         233.2         5.2         1014         18         DU761500         DU761500         DU761500         ASNG3728.           10         222.8         5.0         682         19         AG275418         AG275418 Cyanidios           11         217         4.8         988         18         DU766745         DU766745 ANWIJ3628           C         12         216.2         4.8         1044         18         DU776982         DU767745 ANWIJ3628           C         12         216.2         4.8         1044         18         DU776982         DU767745 ANWIJ3628           C         12         216.2         4.7         527         19         AG947952         DU767982 ASXB1422.           13         216.2         4.7         527         19         AG947952         AG947952         DU767982 ASXB1422.           13         212.8         4.7         560         19         AG9359210								DU780806 ASXB3401.
C         7         235.2         5.2         721         16         BZ560602         BZ550602         pacs2-164           8         233.2         5.2         1014         18         DU762284         DU761500         DU761500         ASNG3728.           10         222.8         5.0         682         19         AG275418         AG275418         Cyanidios           11         217         4.8         988         18         DU766745         DU7676745         DU7676922         ASSB1422.         DU76922         DU76922         DU76922         ASSB1422.         DU76922         ASSB1422.         DU76922         DU76922         ASSB1422.         DU76922         DU76922         DU76922         DU76924         DU76924         DU76924         DU76924         ASCB0204 <td>С</td> <td>5</td> <td>254.2</td> <td>5.7</td> <td>979</td> <td>18</td> <td>DU742577</td> <td>DU742577 ASNC1288.</td>	С	5	254.2	5.7	979	18	DU742577	DU742577 ASNC1288.
8         233.2         5.2         1014         18         DU762284         DU762284         DU76220A         DU761500         ASNG3728.           10         222.8         5.0         682         19         AG275418         AG275418         Cyanidios           11         217         4.8         988         18         DU766745         DU766745         DU766745         ANIM13628           C         12         216.2         4.8         1044         18         DU776982         DU776982 ASXB1422.           13         214         4.8         590         19         AG947952         AG947952         Drosophil           14         213.2         4.7         527         19         AG947500         AG9379210         Drosophil           16         212.8         4.7         696         19         AG939210         AG9393210         Drosophil           16         210.2         4.7         1204         18         ED033682         EDD033682         ED033682         L001, PA         O           17         200.8         4.5         614         19         AG935813         AG9367813         Drosophil           2         18         197         4.4	С	6	239.4	5.3	1021	18	DU739640	DU739640 APKI5317.
9	С	7	235.2	5.2	721	16	BZ560602	BZ560602 pacs2-164
10		8	233.2	5.2	1014	18	DU762284	DU762284 ASNG4109.
11         217         4.8         988         18         DU766745         DU776982         DU76982         DU776982         DU776982         DU776982         DU776982         DU769412         DU766745         DU766745         DU766745         DU766745         DU766745         DU766745         DU766745         DU766745         DU766742         DU766742         DU766742         DU766745         DU7667412		9	228.8	5.1	1009	18	DU761500	DU761500 ASNG3728.
c         12         216.2         4.8         1044         18         DU776982         ASXB1422.           13         214         4.8         590         19         AG947952         AG947950         Drosophil           15         212.8         4.7         696         19         AG939210         AG939210         Drosophil           16         210.2         4.7         1204         18         ED033682         ED033682         LOO1_PA_O           17         200.8         4.5         614         19         AG935813         AG935813         Drosophil           c         18         197         4.4         652         15         AQ990247         AQ990247         Rfc00983           19         197         4.4         612         15         AQ990247         AG27016         Cgonidios           20         196.4         4.4         737         19         AG270164         AG270164         Cyanidios           c         22         194.4         4.3         936         18         DU774013         DU774013         APKG3751.           c         23         191.6         4.3         887         18         DU774013         APKG1440. </td <td></td> <td>10</td> <td>222.8</td> <td>5.0</td> <td>682</td> <td>19</td> <td>AG275418</td> <td>AG275418 Cyanidios</td>		10	222.8	5.0	682	19	AG275418	AG275418 Cyanidios
13         214         4.8         590         19         AG947952         AG947950         Drosophil           14         213.2         4.7         527         19         AG947500         AG939200         Drosophil           16         212.8         4.7         1204         18         ED033682         ED033682         L001_PA_O           17         200.8         4.5         614         19         AG935813         AG935813         Drosophil           1         19         4.4         652         15         AQ990247         AQ935813         Drosophil           20         196.4         4.4         737         19         AG270164         AG270164         Cyanidios           21         195.2         4.3         589         19         AG946673         AG946673         Drosophil           2         194.4         4.3         587         18         DU774013         DU774013         APKG3751.           2         194.6         4.3         887         18         DU74912         DU769412         DU769412         APKG1440.           2         194.6         4.3         887         18         DU74912         DU748280         DU748280         <		11	217	4.8	988	18	DU766745	DU766745 ANIW13628
14         213.2         4.7         527         19         AG947500         AG947500         Drosophil           15         212.8         4.7         696         19         AG939210         AG939210         Drosophil           16         210.2         4.7         1204         18         ED033682         EDD33682 L001_PA_0           17         200.8         4.5         614         19         AG935813         AG935813 Drosophil           1         19         19.4         4.652         15         AQ990247         AQ990247 Rfc00983           19         197         4.4         1143         16         BZ579071         BZ579071 msh2_6169           20         196.4         4.4         737         19         AG946673         AG946673 Drosophil           c         22         194.4         4.3         936         18         DU774013         DU774013 APKG3751.           c         23         191.6         4.3         887         18         DU774013         DU748280         DU748280 ASNC438.b           c         24         188         4.2         783         17         C686610         CL686610 PRIO144c      c         25         183.4         4.1	С	12	216.2	4.8	1044	18	DU776982	
15         212.8         4.7         696         19         AG939210         AG939210         Drosophil           16         210.2         4.7         1204         18         ED033682         ED033682 L001 PA O           17         200.8         4.5         614         19         AG935813         Drosophil           c         18         197         4.4         652         15         AG990247         AG990247         RG00983           19         196.4         4.4         737         19         AG270164         AG270164 Cyanidios           21         195.2         4.3         589         19         AG946673         AG946673 Drosophil           c         22         194.4         4.3         936         18         DU774013         DU774013 APKG3751.           c         23         191.6         4.3         887         18         DU769412         DU769412 APKG1440.           c         24         188         4.2         783         17         CL686610         PRIO144c_           c         25         183.4         4.1         970         18         DU748280         DU748280 ASNC438.b           c         27         180.2		13	214	4.8		19	AG947952	
16         210.2         4.7         1204         18         ED033682         ED033682         L001_PA_0           17         200.8         4.5         614         19         AG935813         AG935813         Drosophil           c         18         197         4.4         652         15         AQ990247         AQ990247 Rfc00983           19         197         4.4         1143         16         BZ579071         BZ579071 msh2_6169           20         196.4         4.4         737         19         AG270164         AG270164 Cyanidios           21         195.2         4.3         589         19         AG946673         AG946673 Drosophil           c         22         194.4         4.3         936         18         DU7769412         DU769412 APKG1440.           c         24         188         4.2         783         17         CL686610         CL686610 PRIO144c_           c         24         188         4.2         783         17         CL686610         CL686610 PRIO144c_           c         25         183.4         4.1         970         18         DU748280         DU748280 ASNC438.b           c         27         1						19		
17         200.8         4.5         614         19         AG935813         AG935813         Drosophil           c         18         197         4.4         652         15         AQ990247         AQ990247         AQ990247         Rfc00983           19         197         4.4         1143         16         BZ579071         BZ579071         msh2_6169           20         196.4         4.4         737         19         AG270164         AG270164         CAG270164         C								
C         18         197         4.4         652         15         AQ990247         AQ990247         Rfc00983           19         197         4.4         1143         16         BZ579071         BZ579071         msh2_6169           20         196.4         4.4         737         19         AG270164         AG270164         Cyanidios           21         195.2         4.3         589         19         AG946673         AG946673         Drosophil           C         22         194.4         4.3         936         18         DU774013         DU769412         DU769412 APKG1440.           C         23         191.6         4.3         887         18         DU769412         DU769412 APKG1440.           C         24         188         4.2         783         17         CL686610         CL686610         PRIO144C.           C         25         183.4         4.1         970         18         DU748280         DU74280         DU7428280 ASNC438.b           C         27         180.2         4.0         633         17         CG896388         CG896388 pastbac02           28         180.2         4.0         864         18 <td< td=""><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td></td<>								
19         197         4.4         1143         16         BZ579071         BZ579071 msh2_6169           20         196.4         4.4         737         19         AG270164         AG270164 Cyanidios           21         195.2         4.3         589         19         AG946673         AG946673 Drosophil           C         22         194.4         4.3         936         18         DU774013         DU774013 APKG3751.           C         23         191.6         4.3         887         18         DU769412         DU769412 APKG1440.           C         24         188         4.2         783         17         CL686610         CL686610 PRIO144c_           C         25         183.4         4.1         970         18         DU748280         DU748280 ASNC438.b           26         180.6         4.0         631         16         BH861083         BH861083 BH861083 BH861083           C         27         180.2         4.0         633         17         CG896388         CG896388 pastbac02           28         180.2         4.0         864         18         DU7325255         DU7325255         APKI1776.           29         180         4.0								
20         196.4         4.4         737         19         AG270164         AG270164         Cyanidios           21         195.2         4.3         589         19         AG946673         AG946673         Drosophil           C         22         194.4         4.3         936         18         DU774013         DU774013         APKG3751.           C         23         191.6         4.3         887         18         DU769412         DU769412         APKG1440.           C         24         188         4.2         783         17         CL686610         DU748280         APKG1440.           C         24         188         4.1         970         18         DU748280         DU748280 ASNC438.b           26         180.6         4.0         631         16         BH861083         BH861083 H3E3T7 We           C         27         180.2         4.0         633         17         CG896388         CG896388 pastbac02           28         180.2         4.0         864         18         DU732525         DU732525         APKT1776.           29         180         4.0         929         18         DU750813         DU750813         A	С							
21         195.2         4.3         589         19         AG946673         AG946673         Drosophil           C         22         194.4         4.3         936         18         DU774013         DU774013         APKG3751.           C         23         191.6         4.3         887         18         DU769412         DU769412         DU76912         DU76912         DU76912         DU76912         DU76912         DU76912         DU76912         DU76912         DU76912         DU748280         DU76912         DU748280         ASNC438.5         E         26         180.4         4.1         970         18         DU748280         DU748280         ASNC438.5         DU748280         ASNC438.5         E         28         180.2         4.0         631         16         BH861083         BH861083         H382377         We         C         27         180.2         4.0         633         17         CG896388         CG896388         pastbac02         28         180.2         4.0         864         18         DU732525         DU732525         DU732525         APK11776.         DU750813         ASNF1671.         30         179.6         4.0         929         18         DU750813         DU750813								
C         22         194.4         4.3         936         18         DU774013         DU774013         APKG3751.           C         23         191.6         4.3         887         18         DU769412         DU769412         APKG1440.           C         24         188         4.2         783         17         CL686610         CL686610         PRIO144c           C         25         183.4         4.1         970         18         DU748280         DU748280 ASNC438.b           26         180.6         4.0         631         16         BH861083         BH861083 H3E3T7 We           C         27         180.2         4.0         633         17         CG896388         CG896388 pastbac02           28         180.2         4.0         864         18         DU732525         DU732525         APKI1776.           29         180         4.0         777         13         DN257460         DN257460 Meso09815           C         30         179.6         4.0         929         18         DU750813         DU750813         ASNF1671.           31         179.2         4.0         712         17         CG896362         CG896362 <t< td=""><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td></t<>								
C         23         191.6         4.3         887         18         DU769412         DU769412         APKG1440.           C         24         188         4.2         783         17         CL686610         CL686610         PRI0144c_           C         25         183.4         4.1         970         18         DU748280         DU748280         ASNC438.b           26         180.6         4.0         631         16         BH861083         BH861083         BH861083         BH861083         HB861083         BH861083         BH861083         BH861083         BH861083         BH861083         BH861083         BH861083         BH861083         BH861083         BG86182         CG896388         pastbac02         DU732525         DU732525         DU732525         DU732525         DU732525         DU732525         DU732525         APKI1776.         DV782014         DU750813         ASNF1671.         ASSA602         CG896362         pastbac02         2G896362         pastbac02         CG896362         pastbac02         CG896362         pastbac02         DU782014         ASXB4014.         ASXB4014.         AG269216         AG269216         AG269216         CG896691         AG269216         CG896691         CG896691         AG269126 <td< td=""><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td></td<>								
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C       33       177.4       3.9       963       18       DU782014       DU782014       ASXB4014.         34       176       3.9       528       19       AG269216       AG269216       Cyanidios         c       35       175.4       3.9       1067       18       DU758748       DU758748       ASNG2090.         c       36       175.2       3.9       1017       18       DU749209       DU749209       ASNC950.b         c       37       174.8       3.9       1013       18       DU782058       DU782058       ASXB4036.         38       174.4       3.9       617       17       CG896695       CG896695       pastbac03         c       39       174.4       3.9       799       18       CZ533942       CZ533942       SRAA-aac8         c       40       172.6       3.8       540       19       AG268676       AG268676       Cyanidios         c       41       172.6       3.8       541       19       AG269121       AG269121       Cyanidios         c       42       172.4       3.8       520       17       CG896610       CG896610       DU787960       APKH2385.								
34       176       3.9       528       19       AG269216       AG269216       Cyanidios         c       35       175.4       3.9       1067       18       DU758748       DU758748       ASNG2090.         c       36       175.2       3.9       1017       18       DU749209       DU749209       ASNC950.b         c       37       174.8       3.9       1013       18       DU782058       DU782058       ASXB4036.         38       174.4       3.9       617       17       CG896695       CG896695       pastbac03         c       39       174.4       3.9       799       18       CZ533942       CZ533942       SRAA-aac8         c       40       172.6       3.8       540       19       AG268676       AG268676       Cyanidios         c       41       172.6       3.8       541       19       AG269121       AG269121       Cyanidios         c       42       172.4       3.8       520       17       CG896610       CG896610       DU787960       APKH2385.         44       170.4       3.8       908       18       DU732151       DU732151       APKI1587.	_							
C       35       175.4       3.9       1067       18       DU758748       DU758748       ASNG2090.         C       36       175.2       3.9       1017       18       DU749209       DU749209       ASNC950.b         C       37       174.8       3.9       1013       18       DU782058       DU782058       ASXB4036.         38       174.4       3.9       617       17       CG896695       CG896695       pastbac03         C       39       174.4       3.9       799       18       CZ533942       CZ533942       SRAA-aac8         C       40       172.6       3.8       540       19       AG268676       AG268676       Cyanidios         C       41       172.6       3.8       541       19       AG269121       AG269121       Cyanidios         C       42       172.4       3.8       520       17       CG896610       CG896610       CG896610       pastbac03         C       43       170.4       3.8       868       18       DU787960       DU787960       APKH2385.         44       170.4       3.8       908       18       DU732151       DU732151       APKI1587.	С							
C       36       175.2       3.9       1017       18       DU749209       DU749209       ASNC950.b         C       37       174.8       3.9       1013       18       DU782058       DU782058       ASXB4036.         38       174.4       3.9       617       17       CG896695       CG896695       pastbac03         C       39       174.4       3.9       799       18       CZ533942       CZ5333942       SRAA-aac8         C       40       172.6       3.8       540       19       AG268676       AG268676       Cyanidios         C       41       172.6       3.8       541       19       AG269121       AG269121       Cyanidios         C       42       172.4       3.8       520       17       CG896610       CG896610       pastbac03         C       43       170.4       3.8       868       18       DU787960       DU787960       APKH2385.         44       170.4       3.8       908       18       DU732151       DU732151       APKI1587.								
C 37 174.8 3.9 1013 18 DU782058 DU782058 ASXB4036. 38 174.4 3.9 617 17 CG896695 CG896695 pastbac03 C 39 174.4 3.9 799 18 CZ533942 CZ533942 SRAA-aac8 C 40 172.6 3.8 540 19 AG268676 AG268676 Cyanidios C 41 172.6 3.8 541 19 AG269121 AG269121 Cyanidios C 42 172.4 3.8 520 17 CG896610 CG896610 pastbac03 C 43 170.4 3.8 868 18 DU787960 DU787960 APKH2385. 44 170.4 3.8 908 18 DU732151 DU732151 APKI1587.								
38 174.4 3.9 617 17 CG896695 CG896695 pastbac03 C 39 174.4 3.9 799 18 CZ533942 CZ533942 SRAA-aac8 C 40 172.6 3.8 540 19 AG268676 AG268676 Cyanidios C 41 172.6 3.8 541 19 AG269121 AG269121 Cyanidios C 42 172.4 3.8 520 17 CG896610 CG896610 pastbac03 C 43 170.4 3.8 868 18 DU787960 DU787960 APKH2385. 44 170.4 3.8 908 18 DU732151 DU732151 APKI1587.								
C       39       174.4       3.9       799       18       CZ533942       CZ533942       SRAA-aac8         C       40       172.6       3.8       540       19       AG268676       AG268676       Cyanidios         C       41       172.6       3.8       541       19       AG269121       AG269121       Cyanidios         C       42       172.4       3.8       520       17       CG896610       CG896610       pastbac03         C       43       170.4       3.8       868       18       DU787960       DU787960       APKH2385.         44       170.4       3.8       908       18       DU732151       DU732151       APKI1587.	C							
C       40       172.6       3.8       540       19       AG268676       AG268676       Cyanidios         C       41       172.6       3.8       541       19       AG269121       AG269121       Cyanidios         C       42       172.4       3.8       520       17       CG896610       CG896610       pastbac03         C       43       170.4       3.8       868       18       DU787960       DU787960       APKH2385.         44       170.4       3.8       908       18       DU732151       DU732151       APKI1587.	-							
C       41       172.6       3.8       541       19       AG269121       AG269121       Cyanidios         C       42       172.4       3.8       520       17       CG896610       CG896610       pastbac03         C       43       170.4       3.8       868       18       DU787960       DU787960       APKH2385.         44       170.4       3.8       908       18       DU732151       DU732151       APKI1587.								
c       42       172.4       3.8       520       17       CG896610       CG896610       pastbac03         c       43       170.4       3.8       868       18       DU787960       DU787960       APKH2385.         44       170.4       3.8       908       18       DU732151       DU732151       APKI1587.								-
C 43 170.4 3.8 868 18 DU787960 DU787960 APKH2385. 44 170.4 3.8 908 18 DU732151 DU732151 APKI1587.								
44 170.4 3.8 908 18 DU732151 DU732151 APKI1587.					-			
	C							
	С							

## ALIGNMENTS

RESULT 1 BH770908

LOCUS BH770908 2768 bp DNA linear GSS 01-MAY-2002 DEFINITION LLMGtag640 MG1363 Random Sequence Tag Library Lactococcus lactis subsp. cremoris genomic, genomic survey sequence.

OM nucleic - nucleic search, using sw model

Run on: November 7, 2007, 02:15:04; Search time 78 Seconds

(without alignments)

15868.232 Million cell updates/sec

Title: US-10-529-319-6

Perfect score: 18.8

Sequence: 1 aarytnggmcctgaagaaat 20

Scoring table: IDENTITY NUCDX

Gapop 10.0 , Gapext 1.0

Searched: 53585215 seqs, 31020513797 residues

Total number of hits satisfying chosen parameters: 107170430

Minimum DB seg length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : EST:\*

1: gb\_est1:\*
2: gb\_est3:\*
3: gb\_est4:\*
4: gb\_est5:\*
5: gb\_est6:\*
6: gb\_htc:\*
7: gb\_est2:\*
8: gb\_est7:\*
9: gb\_est8:\*
10: gb\_est9:\*

11: gb\_est13:\*
12: gb est12:\*

13: gb\_est11:\* 14: gb est10:\*

15: gb\_gss1:\*

16: gb\_gss2:\*

17: gb\_gss3:\*

18: gb gss4:\*

19: gb\_gss5:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result Query

	No.	Score	Match	Length	DB	ID	Description
	1	18.8	100:0	224	2	BE449580	BE449580 EST356339
	2	18.8	100.0	2.49	17	CG616364	CG616364 OST308403
	3	18.8	100.0	267	. 2	BG096334	BG096334 EST460853
	4	18.8	100.0	432	4	BQ111873	BQ111873 EST597449
С	5	18.8	100.0	449	15	AQ339001	AQ339001 HS_5021_A
С	6	18.8	100.0	736	1	AI148550	AI148550 qc68f11.x
	7	18.8	100.0	780	12	EB442713	EB442713 KN6B.1140
	8	18.8	100.0	2768	16	ВН770908	BH770908 LLMGtag64
	9	17.8	94.7		7	BB253849	BB253849 BB253849
	10	17.8	94.7	477	4	BP497438	BP497438 BP497438
	11	17.8	94.7	567	18	DU453884	DU453884 109841577
_	12	17.8	94.7	615	10	CR448915	CR448915 CR448915 CR789429 DKFZp459A
С	13 14	17.8 17.8	94.7 94.7	671 683	10 13	CR789429 DT019698	DT019698 VVI052C01
	15	17.8	94.7	694	9	CN603922	CN603922 USDA FP 1
	1.6	17.8	94.7	707	13	DT944068	DT944068 ZM BFb013
С	17	17.8	94.7	707	13	DV541894	DV541894 ZM BFb023
•	18	17.8	94.7	708	12	EC353178	EC353178 LIVERF091
С	19	17.8	94.7	742	4	BU244836	BU244836 603781034
_	20	17.8	94.7	757	13	DR794581	DR794581 ZM BFb001
С	21	17.8	94.7	775	1.5	BH562959	BH562959 BOGSU18TF
C	22	17.8	94.7	776	12	EB529281	EB529281 304015 Pi
	23	17.8	94.7	1093	19	CNS05GHC	AL336297 Tetraodon
	24	17.8	94.7	1114	17	CL107680	CL107680 ISB1-48K1
С	25	17.8	94.7	1215	13	DN732200	DN732200 CNB63-A03
С	26	17.8	94.7	2478	6	AY105902	AY105902 Zea mays
	27	17.6	93.6	398	5	BY615872	BY615872 BY615872
	28	17.6	93.6	549	13	DT672330	DT672330 s13dLT33D
	29	17.6	93.6	572	13	DT670519	DT670519 s13dLT55A
	30	17.6	93.6	610	9	CN556183	CN556183 tae21f09.
_	31	17.6	93.6 93.6	683 754	13 17	DN603186 CG922594	DN603186 ACAC-aab7 CG922594 MBEHD01TR
С	32 33	17.6 17.6	93.6	838	16	CC856069	CC9522594 MBENDOTTK CC856069 NDL.1716.
С	34	17.6	93.6	970	18	DU748280	DU748280 ASNC438.b
C	35	17.4	92.6	813	19	CNS0128M	ÀL101248 Drosophil
С	36	17.2	91.5	154	2	BE090751	BE090751 PM1-BT072
Ü	37	17.2	91.5	160	17	CE706071	CE706071 tigr-gss-
	38	17.2	91:5	179	2	BE181608	BE181608 CM3-HT063
С	39	17.2	91.5	202	7	AV009565	AV009565 AV009565
	40	17.2	91.5	220	17	CG989474	CG989474 CH240_146
С	41	17.2	91.5	221	15	AZ577061	AZ577061 03e09 Sho
С	42	17.2	91.5	228	7	AW902966	AW902966 CM2-NN102
С	43	17.2	91.5	229	4	BQ353634	BQ353634 CM0-HT091
	44	17.2	91.5	240	1.1	F36208	F36208 HSPD33600 H
	45	17.2	91.5	242	7	BB571249	BB571249 BB571249

# ALIGNMENTS

RESULT 1 BE449580

LOCUS BE449580 224 bp mRNA linear EST 18-MAY-2001 DEFINITION EST356339 L. hirsutum trichome, Cornell University Lycopersicon hirsutum cDNA clone cLHT32E5, mRNA sequence.

OM nucleic - nucleic search, using sw model

Run on: November 7, 2007, 02:15:04; Search time 90 Seconds

(without alignments)

15868.232 Million cell updates/sec

Title: US-10-529-319-7

Perfect score: 22.2

Sequence: 1 tgnartttrtcatcaaccatgtg 23

Scoring table: IDENTITY NUCDX

Gapop 10.0 , Gapext 1.0

Searched: 53585215 seqs, 31020513797 residues

Total number of hits satisfying chosen parameters: 107170430

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : EST:\*

1: gb\_est1:\* 2: gb\_est3:\* 3: gb\_est4:\* 4: gb est5:\* 5: gb est6:\* 6: gb htc:\* gb est2:\* 7: 8: gb est7:\* 9: gb est8:\* 10: gb est9:\* 11: qb est13:\* 12: gb est12:\*

13: gb\_est11:\*
14: gb\_est10:\*

15: gb\_gssl:\*

16: gb\_gss2:\*

17: gb\_gss3:\*

18: gb\_gss4:\*

19: gb\_gss5:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result Query

l	No.	Score	Match	Length	DB	ID	Description
	1	21	94.6	585	4	BP913877	BP913877 BP913877
С	2	21	94.6	642	12	DV678823	DV678823 CGN-16763
С	3	21	94.6	703	12	DV684110	DV684110 CGN-24878
С	4	21	94.6	1318	12	DY280319	DY280319 IC0AAA50D
	5	19.6	88.3	491	3	BI515928	BI515928 BB160020B
С	6	19.6	88.3	734	19	AG443773	AG443773 Mus muscu
С	7	19.6	88.3	756	19	AG561751	AG561751 Mus muscu
С	8	19.4	87.4	275	13	DR973410	DR973410 CHUT007G0
С	9	19.4	87.4		7	AW330550	AW330550 ME000718.
	10	19.4	87.4	363	1	AM157805	AM157805 AM157805
С	11	19.4	87.4	405	8	CA969170	CA969170 CcLX06a21
	12	19.4	87.4	426	1	AJ742017	AJ742017 AJ742017
	13	19.4	87.4	429	13	DR973517	DR973517 CHUT007G0
C	14	19.4	87.4	447	9	CN770050	CN770050 taf75a07. BP708478 BP708478
C	15 16	19.4 19.4	87.4 87.4	458 466	4 11	BP708478 EE281162	EE281162 SAAH-aaa9
С	17	19.4	87.4	488	1	AL672625	AL672625 AL672625
C C	18	19.4	87.4	493	15	AZ929806	AL072023 AL072023 AZ929806 479.dil55
C	19	19.4	87.4	512	4	BU400948	BU400948 603481242
C	20	19.4	87.4	512	19	DE064460	DE064460 Oryzias l
С	21	19.4	87.4	516	4	BU213745	BU213745 603755390
С	22	19.4	87.4	516	15	AZ928670	AZ928670 479.dif14
Ü	23	19.4	87.4	523	19	DE269617	DE269617 Oryzias l
С	24	19.4	87.4	527	19	AG947500	AG947500 Drosophil
C	25	19.4	87.4	531	4	BU405749	BU405749 603484421
	26	19.4	87.4	536	12	EC386480	EC386480 SAAG-aaa0
C	27	19.4	87.4	540	13	DT693234	DT693234 s13dFA25C
	28	19.4	87.4	542	14	CX457104	CX457104 JGI_XZG54
С	29	19.4	87.4	545	4	BU278033	BU278033 603867034
С	30	19.4	87.4	548	13	DT677406	DT677406 s13dFA51D
C	31	19.4	87.4	548	13	DT677502	DT677502 s13dFA53E
С	32	19.4	87.4	548	13	DT677892	DT677892 s13dFA46E
С	33	19.4	87.4	549	4	BU358974	BU358974 603476958
	34	19.4	87.4	550	12	EC386479	EC386479 SAAG-aaa0
С	35	19.4	87.4	550	13	DT675375	DT675375 s13dFA21C
С	36	19.4	87.4	550	13	DT675647	DT675647 s13dFA23G
С	37	19.4	87.4	555	13	DT710379	DT710379 s13dFA45H
С	38	19.4	87.4	561	7	AW641732	AW641732 cm10f10.w
С	39 40	19.4 19.4	87.4 87.4	568 572	9 1	CN120035 AJ394922	CN120035 EC0CAA003 AJ394922 AJ394922
С	40 41	19.4	87.4	573	1	AJ742016	AJ742016 AJ742016
	4 1 4 2	19.4	87.4	576	4	BU415732	BU415732 603669259
C C	43	19.4	87.4	576	5	BY922570	BY922570 BY922570
C	44	19.4	87.4	584	9	CN565309	CN565309 tag23e11.
	45	19.4	87.4	584	10	CV671939	CV671939 RE-3-SJ-L
			· · · <del>-</del>		2		

# ALIGNMENTS

RESULT 1 BP913877

LOCUS BP913877 585 bp mRNA linear EST 09-JUN-2005 DEFINITION BP913877 Adiantum capillus-veneris prothallium Adiantum capillus-veneris cDNA clone YMU001\_000037\_D03, mRNA sequence.

OM nucleic - nucleic search, using sw model

Run on:

November 7, 2007, 02:15:04; Search time 2772 Seconds

(without alignments)

15868.232 Million cell updates/sec

Title:

US-10-529-319-8

Perfect score: 709

Sequence:

1 cgcgaaattccaaacgttgg......tcaccacatggttgatgaca 709

Scoring table: IDENTITY\_NUCDX

Gapop 10.0, Gapext 1.0

Searched:

53585215 seqs, 31020513797 residues

Total number of hits satisfying chosen parameters:

107170430

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100% Listing first 45 summaries

Database:

EST:\*

1: gb\_est1:\*

2: gb\_est3:\*

3: gb\_est4:\*

4: gb\_est5:\*

5: gb\_est6:\*

6: gb\_htc:\*

7: gb\_est2:\*

```
8: gb_est7:*
```

9: gb\_est8:\*

10: gb\_est9:\*

11: gb\_est13:\*

12: gb\_est12:\*

13: gb\_est11:\*

14: gb\_est10:\*

15: gb\_gss1:\*

16: gb\_gss2:\*

17: gb\_gss3:\*

18: gb\_gss4:\*

19: gb\_gss5:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

%

Result Query		
No. Score Match	Length DB ID	Description
1 353 49.8 2	768 16 BH770908	BH770908 LLMGtag64
2 255.6 36.1	988 18 DU766745	DU766745 ANIW13628
c 3 168 23.7	473 19 AG267037	AG267037 Cyanidios
c 4 161.4 22.8	1037 18 DU758598	DU758598 ASNG2002.
c 5 157.6 22.2	451 19 AG269635	AG269635 Cyanidios
c 6 146.2 20.6	954 18 DU795369	DU795369 APKH590.b
7 140.2 19.8	476 19 AG273937	AG273937 Cyanidios
c 8 139.8 19.7	397 19 AG267808	AG267808 Cyanidios
9 136.6 19.3	587 15 BH382180	BH382180 AG-ND-105
c 10 133.6 18.8	683 15 AQ367283	AQ367283 toxb0002I
11 128.8 18.2	759 17 CG026988	CG026988 PGAAC15TR
c 12 128.6 18.1	551 16 BZ9577 <u>1</u> 2	BZ957712 PgH006O15
c 13 127.4 18.0	969 18 DU739459	DU739459 APKI5174.
c 14 126 17.8	716 17 CW441245	CW441245 fsbb001f1
c 15 125.6 17.7	540 19 AG268676	AG268676 Cyanidios

OM nucleic - nucleic search, using sw model

Run on:

November 7, 2007, 02:31:22; Search time 1037 Seconds

(without alignments)

16344.423 Million cell updates/sec

Title:

US-10-529-319-1

Perfect score: 4494.2

Sequence:

1 tcatacttttagagtcagat.....tcaccgctcattccagacac 4523

Scoring table: IDENTITY NUCDX

Gapop 10.0 , Gapext 1.0

Searched:

5155175 segs, 1873024446 residues

Total number of hits satisfying chosen parameters: 10310350

Minimum DB seg length: 0

Maximum DB seg length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

## Issued Patents NA:\*

1: /EMC\_Celerra\_SIDS2/ptodata/1/ina/1 COMB.seq:\* /EMC\_Celerra\_SIDS2/ptodata/1/ina/5\_COMB.seq:\* 2: 3: /EMC\_Celerra\_SIDS2/ptodata/1/ina/6A\_COMB.seq:\* 4: /EMC Celerra\_SIDS2/ptodata/1/ina/6B COMB.seq:\* 5: /EMC Celerra SIDS2/ptodata/1/ina/7A COMB.seq:\* 6: /EMC Celerra SIDS2/ptodata/1/ina/7B\_COMB.seq:\* 7: /EMC Celerra SIDS2/ptodata/1/ina/H COMB.seq:\* /EMC\_Celerra\_SIDS2/ptodata/1/ina/PCTUS\_COMB.seq:\* 9: /EMC Celerra SIDS2/ptodata/1/ina/PP COMB.seq:\* 10: /EMC Celerra SIDS2/ptodata/1/ina/RE COMB.seq: \* 11: /EMC Celerra SIDS2/ptodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Resi	ult No.	Score	% Query Match	Length	DB	ID	Description
 c	 1	 2898	64.5	14672	3	US-08-961-527-111	Sequence 111, App
C	2	2898	64.5	14672	5	US-10-158-844-111	Sequence 111, App
_	3	2470.4	55.0	3651	3	US-09-107-433-1652	Sequence 1652, Ap
	4	2467.2	54.9	3612	3	US-09-583-110-973	Sequence 973, App
	5	2467.2	54.9	3612	5	US-11-028-099A-973	Sequence 973, App
	6	2467.2	54.9	3612	5	US-11-028-291A-973	Sequence 973, App

OM nucleic - nucleic search, using sw model

Run on: November 7, 2007, 08:54:12; Search time 52 Seconds

(without alignments)

9152.710 Million cell updates/sec

Title: US-10-529-319-6

Perfect score: 18.8

Sequence: 1 aarytnggmcctgaagaaat 20

Scoring table: IDENTITY NUCDX

Gapop 10.0 , Gapext 1.0

Searched: 31364175 seqs, 11865555624 residues

Total number of hits satisfying chosen parameters: 62728350

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100%

Listing first 45 summaries

Database: Published Applications NA Main:\*

1: /EMC\_Celerra\_SIDS2/ptodata/1/pubpna/US07\_PUBCOMB.seq:\*
2: /EMC\_Celerra\_SIDS2/ptodata/1/pubpna/US08\_PUBCOMB.seq:\*
3: /EMC\_Celerra\_SIDS2/ptodata/1/pubpna/US09A\_PUBCOMB.seq:\*
4: /EMC\_Celerra\_SIDS2/ptodata/1/pubpna/US09B\_PUBCOMB.seq:\*
5: /EMC\_Celerra\_SIDS2/ptodata/1/pubpna/US09C\_PUBCOMB.seq:\*

6: /EMC\_Celerra\_SIDS2/ptodata/1/pubpna/US09D\_PUBCOMB.seq:\*
7: /EMC\_Celerra\_SIDS2/ptodata/1/pubpna/US10A\_PUBCOMB.seq:\*

8: /EMC\_Celerra\_SIDS2/ptodata/1/pubpna/US10B\_PUBCOMB.seq:\*
9: /EMC\_Celerra\_SIDS2/ptodata/1/pubpna/US10C\_PUBCOMB.seq:\*

10: /EMC\_Celerra\_SIDS2/ptodata/1/pubpna/US10D\_PUBCOMB.seq:\*

11: /EMC\_Celerra\_SIDS2/ptodata/1/pubpna/US10E\_PUBCOMB.seq: \*

12: /EMC\_Celerra\_SIDS2/ptodata/1/pubpna/US10F\_PUBCOMB.seq: \*

13: /EMC\_Celerra\_SIDS2/ptodata/1/pubpna/US10G\_PUBCOMB.seq:\*
14: /EMC\_Celerra\_SIDS2/ptodata/1/pubpna/US10H\_PUBCOMB.seq:\*

14: /EMC\_Celerra\_SIDS2/ptodata/1/pubpna/US10H\_PUBCOMB.seq:\*
15: /EMC\_Celerra\_SIDS2/ptodata/1/pubpna/US10I\_PUBCOMB.seq:\*

16: /EMC Celerra SIDS2/ptodata/1/pubpna/US10J PUBCOMB.seq: \*

17: /EMC\_Celerra\_SIDS2/ptodata/1/pubpna/US10K\_PUBCOMB.seq:\*

18: /EMC\_Celerra\_SIDS2/ptodata/1/pubpna/US11A\_PUBCOMB.seq:\*

19: /EMC\_Celerra\_SIDS2/ptodata/1/pubpna/US11B\_PUBCOMB.seq:\*

20: /EMC\_Celerra\_SIDS2/ptodata/1/pubpna/US11C\_PUBCOMB.seq:\*
21: /EMC\_Celerra\_SIDS2/ptodata/1/pubpna/US11D\_PUBCOMB.seq:\*

22: /EMC\_Celerra\_SIDS2/ptodata/1/pubpna/US11E\_PUBCOMB.seq:\*

23: /EMC\_Celerra\_SIDS2/ptodata/1/pubpna/US11F\_PUBCOMB.seq:\*
24: /EMC\_Celerra\_SIDS2/ptodata/1/pubpna/US11G\_PUBCOMB.seq:\*

25: /EMC\_Celerra\_SIDS2/ptodata/1/pubpna/US11H\_PUBCOMB.seq:\*

26: /EMC\_Celerra\_SIDS2/ptodata/1/pubpna/US11I\_PUBCOMB.seq:\*

27: /EMC Celerra SIDS2/ptodata/1/pubpna/US11J PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

						SUMMARIES	
			96				
Res	ult		Query				
	No.	Score	Match	Length	DB	ID	Description
	1	18.8	100.0	20		US-10-529-319-6	Sequence 6, Appli
С	2	18.8	100.0	162	. 3	US-09-815-242-992	Sequence 992, App
С	3	18.8	100.0	162	9	US-10-282-122A-977	Sequence 977, App
C	4	18.8	100.0	456	3	US-09-815-242-3096	Sequence 3096, Ap
С	5	18.8	100.0	456	9	US-10-282-122A-5649	Sequence 5649, Ap
	6	18.8	100.0	763	9	US-10-398-221-1429	Sequence 1429, Ap
	7	18.8	100.0	891	11	US-10-750-185-42683	Sequence 42683, A
	8	18.8	100.0	891	11	US-10-750-623-42683	Sequence 42683, A
	9	18.8	100.0	891	15	US-10-750-622-42683	Sequence 42683, A
	10	18.8	100.0	2205	14	US-10-434-665-2197	Sequence 2197, Ap
	11	18.8	100.0	3096	14	US-10-529-319-5	Sequence 5, Appli
	12	18.8	100.0	3198	14	US-10-529-319-4	Sequence 4, Appli
	13	18.8	100.0	3405	9	US-10-282-122A-35573	Sequence 35573, A
	14	18.8	100.0	3411	3	US-09-815-242-8349	Sequence 8349, Ap
	15	18.8	100.0	3411	3	US-09-815-242-8716	Sequence 8716, Ap
	16	18.8	100.0	3425	14	US-10-529-319-3	Sequence 3, Appli
	17	18.8	100.0	3474	3	US-09-815-242-3939	Sequence 3939, Ap
	18	18.8	100.0	3537	3	US-09-815-242-4467	Sequence 4467, Ap
	19	18.8	100.0	3549	10	US-10-470-048B-125	Sequence 125, App
	20	18.8	100.0	3549	13	US-10-471-571A-3397	Sequence 3397, Ap
	21	18.8	100.0	3552	9	US-10-282-122A-7607	Sequence 7607, Ap
	22	18.8	100.0	3552	10	US-10-857-625-235	Sequence 235, App
	23	18.8	100.0	3552	15	US-10-859-198-1712	Sequence 1712, Ap
	24	18.8	100.0	3552	15	US-10-859-198-9564	Sequence 9564, Ap
	25	18.8	100.0	3555	9	US-10-282-122A-24519	Sequence 24519, A
	26	18.8	100.0	3561	9	US-10-282-122A-36012	Sequence 36012, A
	27	18.8	100.0	3564	22	US-11-434-137-379	Sequence 379, App
	28	18.8	100.0	3564	22	US-11-434-184-379	Sequence 379, App
	29	18.8	100.0	3564	22	US-11-434-199-379	Sequence 379, App
	30	18.8	100.0	3564	22	US-11-434-203-379	Sequence 379, App
	31	18.8	100.0	3564	22	US-11-434-127-379	Sequence 379, App
	32	18.8	100.0	3567	9	US-10-282-122A-38159	Sequence 38159, A
		18.8	100.0	3567	14	US-10-513-024-723	Sequence 723, App
	33	18.8	100.0	3567	22	US-11-348-413-1550	Sequence 1550, Ap
	34		100.0	3578	3	US-09-974-300-1310	Sequence 1310, Ap
	35	18.8	100.0	3578	23	US-11-203-606-1310	Sequence 1310, Ap
	36	18.8			11	US-10-498-302-1	Sequence 1310, Ap Sequence 1, Appli
	37	18.8	100.0			US-10-369-493-46739	Sequence 1, Appil Sequence 46739, A
	38	18.8	100.0	3582	8		Sequence 40739, A Sequence 42178, A
	39	18.8	100.0	3591	8	US-10-369-493-42178	=
	40	18.8	100.0	3612	9	US-10-282-122A-6253	Sequence 6253, Ap Sequence 6529, Ap
	41	18.8	100.0		3	US-09-815-242-6529	
	42	18.8	100.0		9	US-10-282-122A-21771	Sequence 21771, A
	43	18.8	100.0	3698	10	US-10-488-588-5	Sequence 5, Appli
	44	18.8	100.0		10	US-10-488-588-3	Sequence 3, Appli
	45	18.8	100.0	3851	1.0	US-10-488-588-6	Sequence 6, Appli

OM nucleic - nucleic search, using sw model

Run on: November 7, 2007, 02:31:22; Search time 5 Seconds

(without alignments)

16344.423 Million cell updates/sec

Title: US-10-529-319-7

Perfect score: 22.2

Sequence: 1 tgnartttrtcatcaaccatgtg 23

Scoring table: IDENTITY NUCDX

Gapop 10.0 , Gapext 1.0

Searched: 5155175 seqs, 1873024446 residues

Total number of hits satisfying chosen parameters: 10310350

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents\_NA:\*

1: /EMC\_Celerra\_SIDS2/ptodata/l/ina/1\_COMB.seq:\*
2: /EMC\_Celerra\_SIDS2/ptodata/l/ina/5\_COMB.seq:\*
3: /EMC\_Celerra\_SIDS2/ptodata/l/ina/6A\_COMB.seq:\*
4: /EMC\_Celerra\_SIDS2/ptodata/l/ina/6B\_COMB.seq:\*
5: /EMC\_Celerra\_SIDS2/ptodata/l/ina/7A\_COMB.seq:\*
6: /EMC\_Celerra\_SIDS2/ptodata/l/ina/7B\_COMB.seq:\*
7: /EMC\_Celerra\_SIDS2/ptodata/l/ina/H\_COMB.seq:\*
8: /EMC\_Celerra\_SIDS2/ptodata/l/ina/PCTUS\_COMB.seq:\*

9: /EMC\_Celerra\_SIDS2/ptodata/1/ina/PP\_COMB.seq:\*
10: /EMC\_Celerra\_SIDS2/ptodata/1/ina/RE\_COMB.seq:\*

11: /EMC Celerra SIDS2/ptodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Resu	ult No.	Score	Query Match	Length	DB	ID	Description
C	1	22.2	100.0	271	3	US-08-956-171E-4462	Sequence 4462, Ap
С	2	22.2	100.0	271	3	US-08-781-986A-4462	Sequence 4462, Ap
	3	22.2	100.0	400	3	US-08-956-171E-4154	Sequence 4154, Ap
	4	22.2	100.0	400	3	US-08-781-986A-4154	Sequence 4154, Ap
С	5	22.2	100.0	2205	3	US-09-134-000C-2197	Sequence 2197, Ap
	6	22.2	100.0	14672	3	US-08-961-527-111	Sequence 111, App

OM nucleic - nucleic search, using sw model

Run on: November 7, 2007, 02:31:22; Search time 162 Seconds

(without alignments)

16344.423 Million cell updates/sec

Title: US-10-529-319-8

Perfect score: 709

Sequence: 1 cgcgaaattccaaacgttgg.....tcaccacatggttgatgaca 709

Scoring table: IDENTITY NUCDX

Gapop 10.0 , Gapext 1.0

Searched: 5155175 seqs, 1873024446 residues

Total number of hits satisfying chosen parameters: 10310350

Minimum DB seg length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Issued Patents NA:\*

1: /EMC\_Celerra\_SIDS2/ptodata/1/ina/1\_COMB.seq:\*
2: /EMC\_Celerra\_SIDS2/ptodata/1/ina/5\_COMB.seq:\*
3: /EMC\_Celerra\_SIDS2/ptodata/1/ina/6A\_COMB.seq:\*
4: /EMC\_Celerra\_SIDS2/ptodata/1/ina/6B\_COMB.seq:\*
5: /EMC\_Celerra\_SIDS2/ptodata/1/ina/7A\_COMB.seq:\*
6: /EMC\_Celerra\_SIDS2/ptodata/1/ina/7B\_COMB.seq:\*
7: /EMC\_Celerra\_SIDS2/ptodata/1/ina/H\_COMB.seq:\*
8: /EMC\_Celerra\_SIDS2/ptodata/1/ina/PCTUS\_COMB.seq:\*
9: /EMC\_Celerra\_SIDS2/ptodata/1/ina/PP\_COMB.seq:\*
10: /EMC\_Celerra\_SIDS2/ptodata/1/ina/RE\_COMB.seq:\*
11: /EMC\_Celerra\_SIDS2/ptodata/1/ina/BE\_COMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result		% Query				
No.	Score	Match	Length	DB 	ID	Description
1	566.6	79.9	3612	3	US-09-583-110-973	Sequence 973, App
2	566.6	79.9	3612	5	US-11-028-099A-973	Sequence 973, App
3	566.6	79.9	3612	5	US-11-028-291A-973	Sequence 973, App
4	566.6	79.9	3612	5	US-11-027-878A-973	Sequence 973, App
5	566.6	79.9	3612	5	US-11-027-399-973	Sequence 973, App
6	566.6	79.9	3612	5	US-11-027-877A-973	Sequence 973, App

OM nucleic - nucleic search, using sw model

Run on: November 7, 2007, 08:54:12; Search time 11727 Seconds

(without alignments)

9152.710 Million cell updates/sec

Title: US-10-529-319-1

Perfect score: 4494.2

Sequence: 1 tcatacttttagagtcagat.....tcaccgctcattccagacac 4523

Scoring table: IDENTITY NUCDX

Gapop 10.0, Gapext 1.0

Searched: 31364175 seqs, 11865555624 residues

Total number of hits satisfying chosen parameters: 62728350

Minimum DB seg length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Published Applications NA Main:\*

/EMC\_Celerra\_SIDS2/ptodata/1/pubpna/US07\_PUBCOMB.seq:\* 1: /EMC Celerra SIDS2/ptodata/1/pubpna/US08 PUBCOMB.seq:\* /EMC Celerra SIDS2/ptodata/1/pubpna/US09A PUBCOMB.seq:\* 3: /EMC Celerra SIDS2/ptodata/1/pubpna/US09B PUBCOMB.seq:\* /EMC Celerra SIDS2/ptodata/1/pubpna/US09C PUBCOMB.seq:\* 5: /EMC Celerra SIDS2/ptodata/1/pubpna/US09D PUBCOMB.seq:\* 6: /EMC Celerra SIDS2/ptodata/1/pubpna/US10A PUBCOMB.seq:\* 7: /EMC\_Celerra\_SIDS2/ptodata/1/pubpna/US10B\_PUBCOMB.seq:\* 8: /EMC Celerra SIDS2/ptodata/1/pubpna/US10C PUBCOMB.seq:\* /EMC Celerra SIDS2/ptodata/1/pubpna/US10D PUBCOMB.seq:\* 10: 11: /EMC Celerra SIDS2/ptodata/1/pubpna/US10E PUBCOMB.seq:\* /EMC Celerra SIDS2/ptodata/1/pubpna/US10F PUBCOMB.seq:\* 12: /EMC Celerra SIDS2/ptodata/1/pubpna/US10G PUBCOMB.seq:\* 13: /EMC Celerra SIDS2/ptodata/1/pubpna/US10H PUBCOMB.seq:\* 14: 15: /EMC\_Celerra\_SIDS2/ptodata/1/pubpna/US10I\_PUBCOMB.seq: \* /EMC Celerra SIDS2/ptodata/1/pubpna/US10J PUBCOMB.seq: \* 16: /EMC Celerra\_SIDS2/ptodata/1/pubpna/US10K\_PUBCOMB.seq: \* 17: /EMC Celerra SIDS2/ptodata/1/pubpna/US11A PUBCOMB.seq:\* 18: /EMC Celerra SIDS2/ptodata/1/pubpna/US11B\_PUBCOMB.seq:\* 19: /EMC Celerra SIDS2/ptodata/1/pubpna/US11C PUBCOMB.seq: \* 20: /EMC\_Celerra\_SIDS2/ptodata/1/pubpna/US11D\_PUBCOMB.seq: \* 21: /EMC Celerra SIDS2/ptodata/1/pubpna/US11E PUBCOMB.seq:\* 22: 23: /EMC Celerra SIDS2/ptodata/1/pubpna/US11F PUBCOMB.seq:\* /EMC Celerra SIDS2/ptodata/1/pubpna/US11G PUBCOMB.seq:\* 25: /EMC Celerra SIDS2/ptodata/1/pubpna/US11H PUBCOMB.seq:\* /EMC Celerra SIDS2/ptodata/1/pubpna/US11I PUBCOMB.seq: \* 26: /EMC Celerra SIDS2/ptodata/1/pubpna/US11J PUBCOMB.seq:\* 27:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

			•			SUMMARIES	
			9				
Res	ult		Query			,	
	No.	Score	Match	Length I	DВ	ID	Description
	1	4494.2	100.0	4523	14	US-10-529-319-1	Sequence 1, Appli
С	2	2898	64.5	14672	2	US-08-961-527-111	Sequence 111, App
С	3	2898	64.5	14672	9	US-10-158-844-111	Sequence 111, App
С	4	2898	64.5	14672	27	US-11-563-552-111	Sequence 111, App
С	5	2898		2162598	10		Sequence 4979, Ap
	6	2717		2160266	14		Sequence 1373, Ap
	7	2717		2160266	22		Sequence 10967, A
	8	2717		2160266	22		Sequence 10967, A
	9	2717		2160266	22		Sequence 10967, A
	10	2717		2160266	22		Sequence 10967, A
	11	2717		2160266	22		Sequence 10967, A
	12	2480	55.2	3651	9	US-10-282-122A-37985	Sequence 37985, A
	13	2470.4	55.0	3651	11	US-10-617-320-1652	Sequence 1652, Ap
	14	2467.2	54.9	3612	23	US-11-027-802-973	Sequence 973, App
	15	2467.2	54.9	3612	23	US-11-027-892-973	Sequence 973, App
	16	2467.2	54.9	3612	23	US-11-028-050-973	Sequence 973, App
	17	2467.2	54.9	3612	23	US-11-028-149-973	Seguence 973, App
	18	2467.2	54.9	3612	23	US-11-028-197-973	Sequence 973, App
	19.	2467.2	54.9	3612	23	US-11-028-204-973	Sequence 973, App
	20	2467.2	54.9	3612	23	US-11-028-458-973	Sequence 973, App
	21	2467.2	54.9	3612	23	US-11-524-439-973	Sequence 973, App
	22	2467.2	54.9	3612	23	US-11-524-493-973	Sequence 973, App
	23	2467.2	54.9	3612	23	US-11-524-707-973	Sequence 973, App
	24	2467.2	54.9	3612	23	US-11-524-787-973	Sequence 973, App
	25	2467.2	54.9	3612	23	US-11-524-790-973	Sequence 973, App
	26	2467.2	54.9	3612	23	US-11-524-791-973	Sequence 973, App
	27	2467.2	54.9	3612	23	US-11-524-833-973	Sequence 973, App
	28	2467.2	54.9		23	US-11-524-942-973	Sequence 973, App
	29	2467.2	54.9	3612	23	US-11-524-943-973	Sequence 973, App
	30	2467.2	54.9		23	US-11-524-354-973	Sequence 973, App
	31	2467.2	54.9		23	US-11-028-169-973	Sequence 973, App
	32	2467.2	54.9		23	US-11-524-746-973	Sequence 973, App
	33	2467.2	54.9		25	US-11-524-164-973	Sequence 973, App
	34	2467.2	54.9		25	US-11-524-355-973	Sequence 973, App
	35	2467.2	54.9	3612	25	US-11-607-618-973	Sequence 973, App
	36	2467.2	54.9		25	US-11-607-689-973	Sequence 973, App
	. 37	2467.2	54.9		26	US-11-643-458-973	Sequence 973, App
	38	2467.2	54.9		26	US-11-643-289-973	Sequence 973, App
	39	2467.2	54.9		26	US-11-643-532-973	Sequence 973, App
	40	2467.2	54.9		26	US-11-643-556-973	Sequence 973, App
	41	2467.2	54.9		26	US-11-607-413-973	Sequence 973, App
	42	2467.2	54.9		27	US-11-643-463-973	Sequence 973, App
	43	2462.4	54.8		10	US-10-472-928-4085	Sequence 4085, Ap
	44	2436.6	54.2		22	US-11-348-413-1550	Sequence 1550, Ap
	45	2423.4	53.9	3567	9	US-10-282-122A-38159	Sequence 38159, A

OM nucleic - nucleic search, using sw model

Run on: November 7, 2007, 08:54:12; Search time 52 Seconds

(without alignments)

9152.710 Million cell updates/sec

Title: US-10-529-319-6

Perfect score: 18.8

Sequence: 1 aarytnggmcctgaagaaat 20

Scoring table: IDENTITY NUCDX

Gapop 10.0 , Gapext 1.0

Searched: 31364175 seqs, 11865555624 residues

Total number of hits satisfying chosen parameters: 62728350

Minimum DB seq length: 0

1.

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Published Applications NA Main:\*

/EMC Celerra SIDS2/ptodata/1/pubpna/US07 PUBCOMB.seq: \* /EMC\_Celerra\_SIDS2/ptodata/1/pubpna/US08\_PUBCOMB.seq:\* 2: /EMC Celerra SIDS2/ptodata/1/pubpna/US09A PUBCOMB.seq:\* 3: /EMC Celerra SIDS2/ptodata/1/pubpna/US09B PUBCOMB.seq:\* 4: /EMC Celerra SIDS2/ptodata/1/pubpna/US09C PUBCOMB.seq:\* /EMC Celerra SIDS2/ptodata/1/pubpna/US09D PUBCOMB.seq:\* 6: /EMC Celerra SIDS2/ptodata/1/pubpna/US10A PUBCOMB.seq:\* 7: /EMC Celerra\_SIDS2/ptodata/1/pubpna/US10B PUBCOMB.seq:\* /EMC\_Celerra\_SIDS2/ptodata/1/pubpna/US10C\_PUBCOMB.seq:\* 9: /EMC Celerra SIDS2/ptodata/1/pubpna/US10D PUBCOMB.seq:\* 10: /EMC Celerra SIDS2/ptodata/1/pubpna/US10E PUBCOMB.seq:\* 11: /EMC Celerra SIDS2/ptodata/1/pubpna/US10F PUBCOMB.seq:\* 12: /EMC Celerra SIDS2/ptodata/1/pubpna/US10G PUBCOMB.seq:\* 13: /EMC Celerra SIDS2/ptodata/1/pubpna/US10H PUBCOMB.seq:\* 14: /EMC Celerra\_SIDS2/ptodata/1/pubpna/US10I PUBCOMB.seq: \* 15: /EMC Celerra SIDS2/ptodata/1/pubpna/US10J PUBCOMB.seq: \* 16: /EMC Celerra SIDS2/ptodata/1/pubpna/US10K PUBCOMB.seq: \* 17: /EMC Celerra SIDS2/ptodata/1/pubpna/US11A PUBCOMB.seq: \* /EMC Celerra SIDS2/ptodata/1/pubpna/US11B PUBCOMB.seq:\* 19: /EMC Celerra SIDS2/ptodata/1/pubpna/US11C PUBCOMB.seq: \* 20: /EMC Celerra SIDS2/ptodata/1/pubpna/US11D PUBCOMB.seq: \* 21: /EMC\_Celerra\_SIDS2/ptodata/1/pubpna/US11E\_PUBCOMB.seq: \* 22: /EMC Celerra SIDS2/ptodata/1/pubpna/US11F PUBCOMB.seq: \* 23: /EMC Celerra SIDS2/ptodata/1/pubpna/US11G PUBCOMB.seq: \* 24: /EMC Celerra SIDS2/ptodata/1/pubpna/US11H PUBCOMB.seq:\* 25: /EMC Celerra\_SIDS2/ptodata/1/pubpna/US11I PUBCOMB.seq: \* 26: /EMC Celerra SIDS2/ptodata/1/pubpna/US11J PUBCOMB.seq: \* 27:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

			ક				
Res			Query				
	No.	Score	Match	Length	DB	ID	Description
	 1	18.8	100.0	20	14	US-10-529-319-6	Sequence 6, Appli
С	1 2	18.8	100.0	162	3	US-09-815-242-992	Sequence 992, App
С	3	18.8	100.0	162	9	US-10-282-122A-977	Sequence 977, App
	4	18.8	100.0	456	3	US-09-815-242-3096	Sequence 3096, Ap
C			100.0	456	9	US-10-282-122A-5649	Sequence 5649, Ap
С	5 6	18.8	100.0	763		US-10-282-122A-3649 US-10-398-221-1429	<del>-</del>
	7	$18.8 \\ 18.8$	100.0	891	9 11	US-10-750-185-42683	Sequence 1429, Ap
	8				11		Sequence 42683, A Sequence 42683, A
		18.8		891		US-10-750-623-42683	Sequence 42683, A
	9	18.8	100.0	891	15	US-10-750-622-42683	•
	10	18.8	100.0	2205	14	US-10-434-665-2197	Sequence 2197, Ap
	11	18.8	100.0	3096	14	US-10-529-319-5	Sequence 5, Appli
	12	18.8	100.0	3198	14	US-10-529-319-4	Sequence 4, Appli
	13	18.8	100.0	3405	9	US-10-282-122A-35573	Sequence 35573, A
	14	18.8	100.0	3411	3	US-09-815-242-8349	Sequence 8349, Ap
	15	18.8	100.0	3411	3	US-09-815-242-8716	Sequence 8716, Ap
	16	18.8	100.0	3425	14	US-10-529-319-3	Sequence 3, Appli
	17	18.8	100.0	3474	3	US÷09-815-242-3939	Sequence 3939, Ap
	18	18.8	100.0	3537	3	US-09-815-242-4467	Sequence 4467, Ap
	19	18.8	100.0	3549	10	US-10-470-048B-125	Sequence 125, App
	. 20	18.8	100.0	3549	13	US-10-471-571A-3397	Sequence 3397, Ap
	21	18.8	100.0	3552	9	US-10-282-122A-7607	Sequence 7607, Ap
	22	18.8	100.0	3552	10	US-10-857-625-235	Sequence 235, App
	23	18.8	100.0	3552	15	US-10-859-198-1712	Sequence 1712, Ap
	24	18.8	100.0	3552	15	US-10-859-198-9564	Sequence 9564, Ap
	25	18.8	100.0	3555	9	US-10-282-122A-24519	Sequence 24519, A
	26	18.8	100.0	3561	9	US-10-282-122A-36012	Sequence 36012, A
	27	18.8	100.0	3564	22	US-11-434-137-379	Sequence 379, App
	28	18.8	100.0	3564	22	US-11-434-184-379	Sequence 379, App
	29	18.8	100.0	3564	22	US-11-434-199-379	Sequence 379, App
	30	18.8	100.0	3564	22	US-11-434-203-379	Sequence 379, App
	31	18.8	100.0	3564	22	US-11-434-127-379	Sequence 379, App
	32	18.8	100.0	3567	9	US-10-282-122A-38159	Sequence 38159, A
	33	18.8	100.0	3567	14	US-10-513-024-723	Sequence 723, App
	34	18.8	100.0	3567	22	US-11-348-413-1550	Sequence 1550, Ap
	35	18.8	100.0	3578	3	US-09-974-300-1310	Sequence 1310, Ap
	36	18.8		3578	23		Sequence 1310, Ap
	37	18.8	100.0	3579	11	US-10-498-302-1	Sequence 1, Appli
	38	18.8	100.0	3582	8	US-10-369-493-46739 .	Sequence 46739, A
	39	18.8	100.0	3591	8	US-10-369-493-42178	Sequence 42178, A
	40	18.8	100.0	3612	9	US-10-282-122A-6253	Sequence 6253, Ap
	41	18.8	100.0	3624	3	US-09-815-242-6529	Sequence 6529, Ap
	42	18.8	100.0	3624	9	US-10-282-122A-21771	Sequence 21771, A
	43	18.8	100.0	3698	10	US-10-488-588-5	Sequence 5, Appli
	44	18.8	100.0	3791	10	US-10-488-588-3	Sequence 3, Appli
	45	18.8	100.0	3851	10	US-10-488-588-6	Sequence 6, Appli

OM nucleic - nucleic search, using sw model

Run on: November 7, 2007, 08:54:12; Search time 60 Seconds

(without alignments)

9152.710 Million cell updates/sec

Title: US-10-529-319-7

Perfect score: 22.2

Sequence: 1 tgnartttrtcatcaaccatgtg 23

Scoring table: IDENTITY NUCDX

Gapop 10.0, Gapext 1.0

Searched: 31364175 seqs, 11865555624 residues

Total number of hits satisfying chosen parameters: 62728350

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Published Applications NA Main:\* Database :

/EMC Celerra SIDS2/ptodata/1/pubpna/US07 PUBCOMB.seq:\* /EMC\_Celerra\_SIDS2/ptodata/1/pubpna/US08\_PUBCOMB.seq: \* /EMC Celerra SIDS2/ptodata/1/pubpna/US09A PUBCOMB.seq:\* /EMC Celerra SIDS2/ptodata/1/pubpna/US09B PUBCOMB.seq:\* 4: /EMC Celerra SIDS2/ptodata/1/pubpna/US09C PUBCOMB.seq:\* /EMC\_Celerra\_SIDS2/ptodata/1/pubpna/US09D\_PUBCOMB.seq:\* /EMC Celerra SIDS2/ptodata/1/pubpna/US10A PUBCOMB.seq:\* 7: /EMC Celerra SIDS2/ptodata/1/pubpna/US10B PUBCOMB.seq:\* /EMC Celerra SIDS2/ptodata/1/pubpna/US10C PUBCOMB.seq:\* /EMC Celerra SIDS2/ptodata/1/pubpna/US10D PUBCOMB.seq:\* 10: 11: /EMC Celerra SIDS2/ptodata/1/pubpna/US10E PUBCOMB.seq:\* /EMC\_Celerra\_SIDS2/ptodata/1/pubpna/US10F\_PUBCOMB.seq:\* 12: /EMC Celerra\_SIDS2/ptodata/1/pubpna/US10G PUBCOMB.seq:\* 13: /EMC Celerra SIDS2/ptodata/1/pubpna/US10H PUBCOMB.seq:\* 14: 15: /EMC\_Celerra\_SIDS2/ptodata/1/pubpna/US10I\_PUBCOMB.seq: \* 16: /EMC Celerra SIDS2/ptodata/1/pubpna/US10J PUBCOMB.seq:\* /EMC\_Celerra\_SIDS2/ptodata/1/pubpna/US10K\_PUBCOMB.seq:\* 17: /EMC Celerra SIDS2/ptodata/1/pubpna/US11A PUBCOMB.seq:\* /EMC\_Celerra\_SIDS2/ptodata/1/pubpna/US11B\_PUBCOMB.seq: \* 19: /EMC\_Celerra\_SIDS2/ptodata/1/pubpna/US11C\_PUBCOMB.seq: \* 20: /EMC Celerra SIDS2/ptodata/1/pubpna/US11D PUBCOMB.seq:\* /EMC\_Celerra\_SIDS2/ptodata/1/pubpna/US11E\_PUBCOMB.seq: \* 22: /EMC Celerra SIDS2/ptodata/1/pubpna/US11F PUBCOMB.seq:\* 23: /EMC\_Celerra\_SIDS2/ptodata/1/pubpna/US11G\_PUBCOMB.seq:\* /EMC Celerra SIDS2/ptodata/1/pubpna/US11H PUBCOMB.seq: \* 26: /EMC\_Celerra\_SIDS2/ptodata/1/pubpna/US11I PUBCOMB.seq:\* /EMC Celerra SIDS2/ptodata/1/pubpna/US11J PUBCOMB.seq: \* 27:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

No. Score Match Length DB ID Description  1 22.2 100.0 23 14 US-10-529-319-7 Sequence 7, Appli 2 22.2 100.0 158 3 US-09-815-242-474 Sequence 49, Appl 3 22.2 100.0 158 3 US-09-815-242-474 Sequence 2058, Ap 5 22.2 100.0 158 9 US-10-282-122A-488 Sequence 2058, Ap 6 22.2 100.0 166 3 US-09-815-242-3017 Sequence 3017, Appli 8 22.2 100.0 166 3 US-09-815-242-3017 Sequence 3017, Ap 8 22.2 100.0 166 9 US-10-282-122A-4567 Sequence 3017, Ap 9 22.2 100.0 166 9 US-10-282-122A-5591 Sequence 3017, Ap 10 22.2 100.0 166 9 US-10-282-122A-5936 Sequence 3017, Ap 11 22.2 100.0 202 9 US-10-282-122A-5936 Sequence 3017, Ap 11 22.2 100.0 202 9 US-10-282-122A-5936 Sequence 3017, Ap 22.2 100.0 202 9 US-10-282-122A-5936 Sequence 3017, Ap 22.2 100.0 202 9 US-10-282-122A-5936 Sequence 2058, Ap 22.2 100.0 202 9 US-10-282-122A-5936 Sequence 2059, Ap 22.2 100.0 271 9 US-10-329-624-4462 Sequence 4462, Ap 22.2 100.0 271 9 US-10-329-624-4462 Sequence 4462, Ap 22.2 100.0 271 9 US-10-329-624-4462 Sequence 4462, Ap 22.2 100.0 271 14 US-10-807-556-4462 Sequence 4462, Ap 22.2 100.0 274 9 US-10-282-122A-366 Sequence 366, App 22.2 100.0 274 9 US-10-282-122A-366 Sequence 366, Ap 22.2 100.0 274 9 US-10-282-122A-366 Sequence 366, Ap 22.2 100.0 275 9 US-10-282-122A-617 Sequence 367, App 22.2 100.0 275 9 US-10-282-122A-617 Sequence 367, App 22.2 100.0 275 9 US-10-282-122A-617 Sequence 367, App 22.2 100.0 321 3 US-09-815-242-442 Sequence 4154, Ap 22.2 100.0 321 3 US-09-815-242-445 Sequence 4154, Ap 22.2 100.0 321 3 US-09-815-242-445 Sequence 4154, Ap 22.2 100.0 321 3 US-09-815-242-467 Sequence 4154, Ap 22.2 100.0 3549 10 US-10-434-655-2197 Sequence 4154, Ap 22.2 100.0 3549 10 US-10-282-122A-617 Sequence 4154, Ap 22.2 100.0 3549 10 US-10-48-1144 Sequence 4154, Ap 22.2 100.0 3552 10 US-10-89-198-916 Sequence 3399, Ap 232.2 100.0 3552 10 US-10-89-198-916 Sequence 3399, Ap 232.2 100.0 3552 15 US-10-89-198-916 Sequence 3399, Ap 232.2 100.0 3564 22 US-11-434-137-379 Sequence 379, App 24 3 22.2 100.0 3564 22 US-11-434-193-379 Sequence 379, App 24 3 22.2 100.0 3564 22	_	3.1		ક				
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c 28         22.2         100.0         2205         14         US-10-434-665-2197         Sequence 2197, Ap           c 29         22.2         100.0         3096         14         US-10-529-319-5         Sequence 5, Appli           c 30         22.2         100.0         3411         3         US-09-815-242-8349         Sequence 8349, Ap           c 31         22.2         100.0         3411         3         US-09-815-242-8716         Sequence 8716, Ap           c 32         22.2         100.0         3474         3         US-09-815-242-3939         Sequence 3939, Ap           c 33         22.2         100.0         3537         3         US-09-815-242-4467         Sequence 4467, Ap           c 34         22.2         100.0         3549         10         US-10-470-048B-125         Sequence 125, App           c 35         22.2         100.0         3549         13         US-10-471-571A-3397         Sequence 3397, Ap           c 36         22.2         100.0         3552         9         US-10-857-625-235         Sequence 7607, Ap           c 37         22.2         100.0         3552         15         US-10-859-198-1712         Sequence 235, App           c 40         22.2         <								
c       29       22.2       100.0       3096       14       US-10-529-319-5       Sequence 5, Appli         c       30       22.2       100.0       3411       3       US-09-815-242-8349       Sequence 8349, Ap         c       31       22.2       100.0       3411       3       US-09-815-242-8716       Sequence 8716, Ap         c       32       22.2       100.0       3474       3       US-09-815-242-3939       Sequence 3939, Ap         c       33       22.2       100.0       3537       3       US-09-815-242-4467       Sequence 4467, Ap         c       34       22.2       100.0       3549       10       US-10-470-048B-125       Sequence 125, App         c       35       22.2       100.0       3549       13       US-10-471-571A-3397       Sequence 3397, Ap         c       36       22.2       100.0       3552       9       US-10-282-122A-7607       Sequence 7607, Ap         c       37       22.2       100.0       3552       15       US-10-859-198-1712       Sequence 235, App         c       39       22.2       100.0       3552       15       US-10-859-198-9564       Sequence 9564, Ap         c       40 </td <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td>· · · · · · · · · · · · · · · · · · ·</td>								· · · · · · · · · · · · · · · · · · ·
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c       32       22.2       100.0       3474       3       US-09-815-242-3939       Sequence 3939, Ap         c       33       22.2       100.0       3537       3       US-09-815-242-4467       Sequence 4467, Ap         c       34       22.2       100.0       3549       10       US-10-470-048B-125       Sequence 125, App         c       35       22.2       100.0       3549       13       US-10-471-571A-3397       Sequence 3397, Ap         c       36       22.2       100.0       3552       9       US-10-282-122A-7607       Sequence 7607, Ap         c       37       22.2       100.0       3552       10       US-10-857-625-235       Sequence 235, App         c       38       22.2       100.0       3552       15       US-10-859-198-1712       Sequence 1712, Ap         c       39       22.2       100.0       3552       15       US-10-859-198-9564       Sequence 9564, Ap         c       40       22.2       100.0       3555       9       US-10-282-122A-24519       Sequence 24519, A         c       41       22.2       100.0       3564       22       US-11-434-137-379       Sequence 379, App         c								
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c       35       22.2       100.0       3549       13       US-10-471-571A-3397       Sequence 3397, Ap         c       36       22.2       100.0       3552       9       US-10-282-122A-7607       Sequence 7607, Ap         c       37       22.2       100.0       3552       10       US-10-857-625-235       Sequence 235, App         c       38       22.2       100.0       3552       15       US-10-859-198-1712       Sequence 1712, Ap         c       39       22.2       100.0       3552       15       US-10-859-198-9564       Sequence 9564, Ap         c       40       22.2       100.0       3555       9       US-10-282-122A-24519       Sequence 24519, A         c       41       22.2       100.0       3561       9       US-10-282-122A-36012       Sequence 36012, A         c       42       22.2       100.0       3564       22       US-11-434-137-379       Sequence 379, App         c       43       22.2       100.0       3564       22       US-11-434-184-379       Sequence 379, App         c       44       22.2       100.0       3564       22       US-11-434-199-379       Sequence 379, App								
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c       39       22.2       100.0       3552       15       US-10-859-198-9564       Sequence 9564, Ap         c       40       22.2       100.0       3555       9       US-10-282-122A-24519       Sequence 24519, A         c       41       22.2       100.0       3561       9       US-10-282-122A-36012       Sequence 36012, A         c       42       22.2       100.0       3564       22       US-11-434-137-379       Sequence 379, App         c       43       22.2       100.0       3564       22       US-11-434-184-379       Sequence 379, App         c       44       22.2       100.0       3564       22       US-11-434-199-379       Sequence 379, App								
c       40       22.2       100.0       3555       9       US-10-282-122A-24519       Sequence 24519, A         c       41       22.2       100.0       3561       9       US-10-282-122A-36012       Sequence 36012, A         c       42       22.2       100.0       3564       22       US-11-434-137-379       Sequence 379, App         c       43       22.2       100.0       3564       22       US-11-434-184-379       Sequence 379, App         c       44       22.2       100.0       3564       22       US-11-434-199-379       Sequence 379, App	С							
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OM nucleic - nucleic search, using sw model

Run on: November 7, 2007, 08:54:12; Search time 1838 Seconds

(without alignments)

9152.710 Million cell updates/sec

Title: US-10-529-319-8

Perfect score: 709

Sequence: 1 cgcgaaattccaaacgttgg.....tcaccacatggttgatgaca 709

Scoring table: IDENTITY NUCDX

Gapop 10.0 , Gapext 1.0

Searched: 31364175 seqs, 11865555624 residues

Total number of hits satisfying chosen parameters: 62728350

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

22:

23:

25:

26:

27:

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA Main:\*

/EMC Celerra SIDS2/ptodata/1/pubpna/US07 PUBCOMB.seq:\* /EMC\_Celerra\_SIDS2/ptodata/1/pubpna/US08\_PUBCOMB.seq:\* 2: /EMC Celerra SIDS2/ptodata/1/pubpna/US09A PUBCOMB.seq:\* 3: /EMC\_Celerra\_SIDS2/ptodata/1/pubpna/US09B PUBCOMB.seq:\* .4: /EMC Celerra SIDS2/ptodata/1/pubpna/US09C PUBCOMB.seq:\* 5: /EMC Celerra SIDS2/ptodata/1/pubpna/US09D PUBCOMB.seq:\* 6: /EMC Celerra SIDS2/ptodata/1/pubpna/US10A PUBCOMB.seq:\* 7: /EMC Celerra SIDS2/ptodata/1/pubpna/US10B PUBCOMB.seq: \* /EMC Celerra SIDS2/ptodata/1/pubpna/US10C PUBCOMB.seq:\* /EMC Celerra SIDS2/ptodata/1/pubpna/US10D PUBCOMB.seq:\* 10: /EMC Celerra SIDS2/ptodata/1/pubpna/US10E PUBCOMB.seq:\* /EMC\_Celerra\_SIDS2/ptodata/1/pubpna/US10F\_PUBCOMB.seq:\* 12: /EMC\_Celerra\_SIDS2/ptodata/1/pubpna/US10G\_PUBCOMB.seq:\* 13: /EMC Celerra SIDS2/ptodata/1/pubpna/US10H PUBCOMB.seq:\* 14: 15: /EMC Celerra SIDS2/ptodata/1/pubpna/US10I\_PUBCOMB.seq: \* /EMC Celerra SIDS2/ptodata/1/pubpna/US10J PUBCOMB.seq:\* 16: /EMC Celerra SIDS2/ptodata/1/pubpna/US10K PUBCOMB.seq:\* 17: /EMC Celerra SIDS2/ptodata/1/pubpna/US11A PUBCOMB.seq:\* 18: /EMC Celerra SIDS2/ptodata/1/pubpna/US11B PUBCOMB.seq:\* 19: /EMC Celerra SIDS2/ptodata/1/pubpna/US11C PUBCOMB.seq: \* 20: 21: /EMC\_Celerra\_SIDS2/ptodata/1/pubpna/US11D\_PUBCOMB.seq: \*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	No.	Score	Match	Length		ID	Description
	1	709	100.0	709	14	· US-10-529-319-8	Sequence 8, Appli
	2	619	87.3	4118	1.4	US-10-529-319-2	Sequence 2, Appli
С	3	593.8	83.8	728	1.4	US-10-529-319-21	Sequence 21, Appl
	4	568.2	80.1	3471 <sup>-</sup>	3	US-09-815-242-9089	Sequence 9089, Ap
	5	568.2	80.1	3651	9	US-10-282-122A-37985	Sequence 37985, A
	. 6	566.6	79.9	3612	23	US-11-027-802-973	Sequence 973, App
	7	566.6	79.9	3612	23	US-11-027-892-973	Sequence 973, App
	8	566.6	79.9	3612	23	US-11-028-050-973	Sequence 973, App
	9	566.6	79.9	3612	23	US-11-028-149-973	Sequence 973, App
	10	566.6	79.9	3612	23	US-11-028-197-973	Sequence 973, App
	11	566.6	79.9	3612	23	US-11-028-204-973	Sequence 973, App
	12	566.6	79.9	3612	23	US-11-028-458-973	Sequence 973, App
	13	566.6	79.9	3612	23	US-11-524-439-973	Sequence 973, App
	14	566.6	79.9	3612	23	US-11-524-493-973	Sequence 973, App
	15	566.6	79.9	3612	23	US-11-524-707-973	Sequence 973, App
	16	566.6	79.9	3612	23	US-11-524-787-973	Sequence 973, App
	17	566.6	79.9	3612	23	US-11-524-790-973	Sequence 973, App
	18	566.6	79.9	3612	23	US-11-524-791-973	Sequence 973, App
	19	566.6	79.9	3612	23	US-11-524-833-973	Sequence 973, App
	20	566.6	79.9	3612	23	US-11-524-942-973	Sequence 973, App
	21	566.6	79.9	3612	23	US-11-524-943-973	Sequence 973, App
	22	566.6	79.9	3612	23	US-11-524-354-973	Sequence 973, App
	23	566.6	79.9	3612	23	US-11-028-169-973	Sequence 973, App
	24	566.6	79.9	3612	23	US-11-524-746-973	Sequence 973, App
	25	566.6	79.9	3612	25	US-11-524-164-973	Sequence 973, App
	26	566.6	79.9	3612	25	US-11-524-355-973	Sequence 973, App
	27	566.6	79.9	3612	25	US-11-607-618-973	Sequence 973, App
	28	566.6	79.9	3612	25	US-11-607-689-973	Sequence 973, App
	29	566.6	79.9	3612	26	US-11-643-458-973	Sequence 973, App
	30	566.6	79.9	3612	26	US-11-643-289-973	Sequence 973, App
	31	566.6	79.9	3612	26	US-11-643-532-973	Sequence 973, App
	32	566.6	79.9	3612	26	US-11-643-556-973	Sequence 973, App
	33	566.6	79.9	3612	26	US-11-607-413-973	Sequence 973, App
	34	566.6	79.9	3612	27	US-11-643-463-973	Sequence 973, App
	35	566.6	79.9	3651	11	US-10-617-320-1652	Sequence 1652, Ap
	36	563.4	79.5		10		Sequence 4085, Ap
Ç	37	563.4	79.5	14672	2	US-08-961-527-111	Sequence 111, App
C	38	563.4	79.5	14672	9	US-10-158-844-111	Sequence 111, App
С	39	563.4	79.5	14672	27	US-11-563-552-111	Sequence 111, App
С	40	563.4		2162598			Sequence 4979, Ap
С	41	561	79.1	728	14	US-10-529-319-10	Sequence 10, Appl
C	42	555.4	78.3	728	14	US-10-529-319-19	Sequence 19, Appl
С	43	553	78.0	725	14	US-10-529-319-9	Sequence 9, Appli
	44	546.6	77.1	3576	22	US-11-348-413-6399	Sequence 6399, Ap
С	45	545.8	77.0	714	14	US-10-529-319-23	Sequence 23, Appl

mphn-1

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OM nucleic - nucleic search, using sw model

November 7, 2007, 02:58:45; Search time 1155 Seconds Run on:

(without alignments)

2488.446 Million cell updates/sec

Title: US-10-529-319-1

Perfect score: 4494.2

1 tcatacttttagagtcagat.....tcaccgctcattccagacac 4523 Sequence:

Scoring table: IDENTITY NUCDX

Gapop 10.0 , Gapext 1.0

Searched: 2606767 seqs, 317719116 residues

Total number of hits satisfying chosen parameters: 5213534

Minimum DB seg length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

ð

Maximum Match 100%

Listing first 45 summaries

Published Applications NA\_New: \* Database :

1: /EMC Celerra SIDS2/ptodata/1/pubpna/US09\_NEW\_PUB.seq:\*

/EMC\_Celerra\_SIDS2/ptodata/1/pubpna/US06\_NEW\_PUB.seq: \*

3: /EMC Celerra SIDS2/ptodata/1/pubpna/US07 NEW PUB.seq:\*

/EMC Celerra SIDS2/ptodata/1/pubpna/US08 NEW PUB.seq:\*

/EMC\_Celerra\_SIDS2/ptodata/1/pubpna/PCT NEW PUB.seq:\*

6: /EMC Celerra SIDS2/ptodata/1/pubpna/US10 NEW PUB.seq:\*

/EMC Celerra SIDS2/ptodata/1/pubpna/US11 NEW PUB.seq:\* 7:

/EMC\_Celerra\_SIDS2/ptodata/1/pubpna/US11\_NEW\_PUB.seq1:\* /EMC Celerra SIDS2/ptodata/1/pubpna/US60 NEW PUB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Resul No		Score	Query Match	Length I	DB	ID	Description
	1	2467.2	54.9	3612	7	US-11-803-079-973	Sequence 973, App
	2	2467.2	54.9	3612	7	US-11-803-173-973	Sequence 973, App
	3	2467.2	54.9	3612	8	US-11-796-730-973	Sequence 973, App
	4	455.6	10.1	3678	7	US-11-803-079-976	Sequence 976, App
	5	455.6	10.1	3678	7	US-11-803-173-976	Sequence 976, App
	6	455.6	10.1	3678	8	US-11-796-730-976	Sequence 976, App
	7	411	9.1	2242716	7	US-11-711-740-1	Sequence 1, Appli
С	8	234.4	5.2	348	7	US-11-803-079-974	Sequence 974, App

rapbn-6

## GenCore version 6.2.1 Copyright (c) 1993 - 2007 Biocceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 7, 2007, 02:58:45; Search time 5 Seconds

(without alignments)

2488.446 Million cell updates/sec

Title: US-10-529-319-6

Perfect score: 18.8

Sequence: 1 aarytnggmcctgaagaaat 20

Scoring table: IDENTITY NUCDX

Gapop 10.0 , Gapext 1.0

Searched: 2606767 seqs, 317719116 residues

Total number of hits satisfying chosen parameters: 5213534

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Published Applications NA New:\*

1: /EMC\_Celerra\_SIDS2/ptodata/1/pubpna/US09\_NEW\_PUB.seq:\*

2: /EMC Celerra SIDS2/ptodata/1/pubpna/US06 NEW PUB.seq:\*

3: /EMC Celerra\_SIDS2/ptodata/1/pubpna/US07 NEW PUB.seq:\*

4: /EMC Celerra SIDS2/ptodata/1/pubpna/US08 NEW PUB.seq:\*

5: /EMC Celerra SIDS2/ptodata/1/pubpna/PCT NEW PUB.seq:\*

6: /EMC Celerra SIDS2/ptodata/1/pubpna/US10 NEW PUB.seq:\*

7: /EMC Celerra SIDS2/ptodata/1/pubpna/US11 NEW PUB.seq:\*

3: /EMC\_Celerra\_SIDS2/ptodata/1/pubpna/US11 NEW PUB.seq1:\*

9: /EMC Celerra SIDS2/ptodata/1/pubpna/US60 NEW PUB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

oult Query No. Score Match Length DB ID	Description
1 17.8 94.7 1153 8 US-11-514-704-10707 2 17.8 94.7 2488 8 US-11-514-704-10710 3 17.6 93.6 348 7 US-11-803-079-974 4 17.6 93.6 348 7 US-11-803-173-974 5 17.6 93.6 348 8 US-11-796-730-974 6 17.6 93.6 3612 7 US-11-803-079-973 7 17.6 93.6 3612 7 US-11-803-173-973 8 17.6 93.6 3612 8 US-11-796-730-973	Sequence 10707, A Sequence 10710, A Sequence 974, App Sequence 974, App Sequence 974, App Sequence 973, App Sequence 973, App Sequence 973, App

OM nucleic - nucleic search, using sw model

Run on: November 7, 2007, 02:58:45; Search time 6 Seconds

(without alignments)

2488.446 Million cell updates/sec

Title: US-10-529-319-7

Perfect score: 22.2

Sequence: 1 tgnartttrtcatcaaccatgtg 23

Scoring table: IDENTITY NUCDX

Gapop 10.0 , Gapext 1.0

Searched: 2606767 segs, 317719116 residues

Total number of hits satisfying chosen parameters: 5213534

Minimum DB seg length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Published Applications NA New:\*

1: /EMC\_Celerra\_SIDS2/ptodata/1/pubpna/US09\_NEW\_PUB.seq:\*
2: /EMC\_Celerra\_SIDS2/ptodata/1/pubpna/US06\_NEW\_PUB.seq:\*
3: /EMC\_Celerra\_SIDS2/ptodata/1/pubpna/US07\_NEW\_PUB.seq:\*
4: /EMC\_Celerra\_SIDS2/ptodata/1/pubpna/US08\_NEW\_PUB.seq:\*
5: /EMC\_Celerra\_SIDS2/ptodata/1/pubpna/PCT\_NEW\_PUB.seq:\*
6: /EMC\_Celerra\_SIDS2/ptodata/1/pubpna/US10\_NEW\_PUB.seq:\*

7: /EMC\_Celerra\_SIDS2/ptodata/1/pubpna/US11\_NEW\_PUB.seq:\*
8: /EMC\_Celerra\_SIDS2/ptodata/1/pubpna/US11\_NEW\_PUB.seq1:\*

9: /EMC\_Celerra\_SIDS2/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Res	ult No.	Score	Query Match	Length	DB	ID	Description
 c	1	20.6	92.8	3612	 7	US-11-803-079-973	Sequence 973, App
С	2	20.6	92.8	3612	7	US-11-803-173-973	Sequence 973, App
C	3	20.6	92.8	3612	8	US-11-796-730-973	Sequence 973, App
	4	18	81.1	681	6	US-10-529-351A-3924	Sequence 3924, Ap
С	5	1.8	81.1	1486	6	US-10-438-246-4308	Sequence 4308, Ap
С	6	17.8	80.2	1562	8	US-11-514-704-13511	Sequence 13511, A
	7	17.8	80.2	169659	7	US-11-403-116-1165	Sequence 1165, Ap
	8	17.4	78.4	336	7	US-11-239-610A-39312	Sequence 39312, A

rnpbn-8

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OM nucleic - nucleic search, using sw model

Run on: November 7, 2007, 02:58:45; Search time 181 Seconds

(without alignments)

2488.446 Million cell updates/sec

Title: US-10-529-319-8

Perfect score: 709

Sequence: 1 cqcqaaattccaaacqttqq.....tcaccacatqqttqatqaca 709

Scoring table: IDENTITY NUCDX

Gapop 10.0 , Gapext 1.0

Searched: 2606767 seqs, 317719116 residues

Total number of hits satisfying chosen parameters: 5213534

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

1:

Maximum Match 100%

Listing first 45 summaries

Database: Published Applications NA New:\*

2: /EMC\_Celerra\_SIDS2/ptodata/1/pubpna/US06\_NEW\_PUB.seq:\*
3: /EMC\_Celerra\_SIDS2/ptodata/1/pubpna/US07\_NEW\_PUB.seq:\*
4: /EMC\_Celerra\_SIDS2/ptodata/1/pubpna/US08\_NEW\_PUB.seq:\*
5: /EMC\_Celerra\_SIDS2/ptodata/1/pubpna/PCT\_NEW\_PUB.seq:\*

/EMC Celerra SIDS2/ptodata/1/pubpna/US09 NEW PUB.seq:\*

6: /EMC\_Celerra\_SIDS2/ptodata/1/pubpna/US10\_NEW\_PUB.seq:\*

7: /EMC\_Celerra\_SIDS2/ptodata/1/pubpna/US11\_NEW\_PUB.seq:\*
8: /EMC\_Celerra\_SIDS2/ptodata/1/pubpna/US11\_NEW\_PUB.seq1:\*

9: /EMC Celerra SIDS2/ptodata/1/pubpna/US60 NEW PUB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Re:	sult No.	Score	% Query Match	Length	DB	ID	Description
	1	566.6	79.9	3612	7	US-11-803-079-973	Sequence 973, App
	2	566.6	79.9	3612	7	US-11-803-173-973	Sequence 973, App
	3	566.6	79.9	3612	8	US-11-796-730-973	Sequence 973, App
С	4	234	33.0	348	7	US-11-803-079-974	Sequence 974, App
С	5	234	33.0	348	7	US-11-803-173-974	Sequence 974, App
С	6	234	33.0	348	8	US-11-796-730-974	Sequence 974, App
	7	130.4	18.4	2242716	7	US-11-711-740-1	Sequence 1, Appli
	8	66	9.3	1562	8	US-11-514-704-13511	Sequence 13511, A